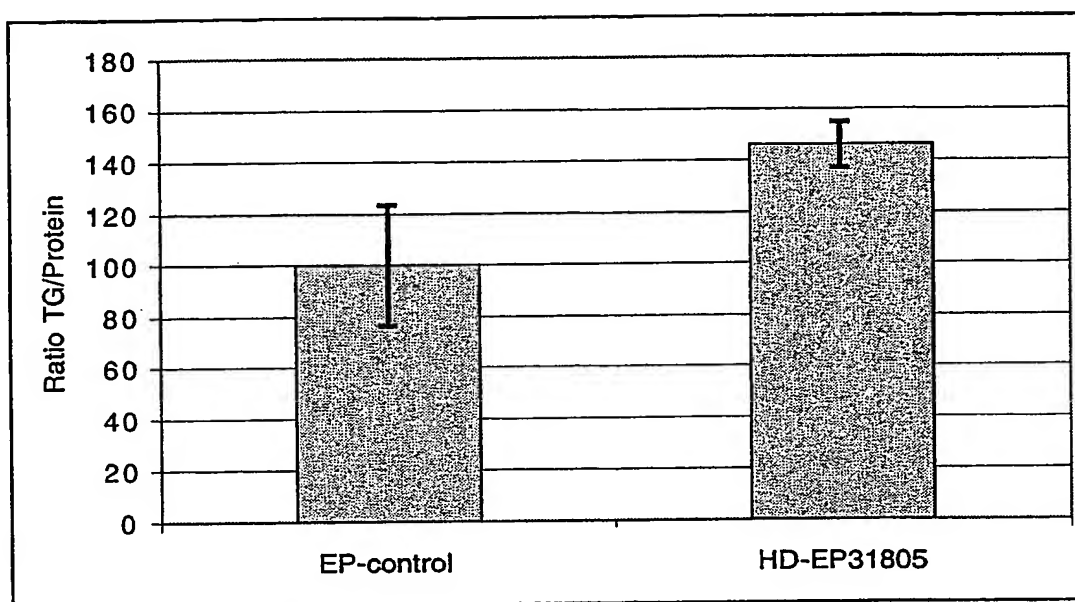


Figure 1. Triglyceride content of a *Drosophila* CG7956 (GadFly Accession Number) mutant



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Figure 2. Molecular organization of the CG7956 gene (GadFly Accession Number)

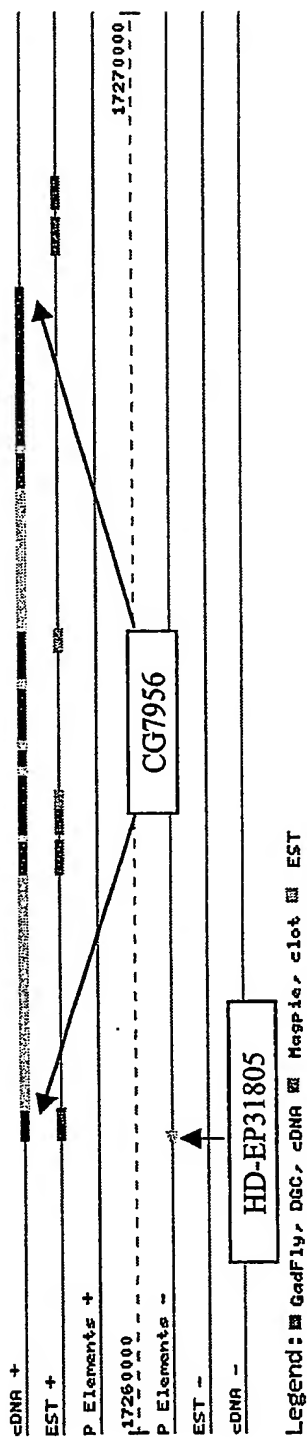


Figure 3. BLASTP results for CG7956 (GadFly Accession Number)**Homology to human protein NP_055752.1 (GenBank Accession Number)**

ref|NP_055752.1| (NM_014937) KIAA0966 protein [Homo sapiens]
Length = 1132

Score = 573 bits (1477), Expect = e-162

Identities = 354/972 (36%), Positives = 514/972 (52%), Gaps = 114/972 (11%)

Query: 1 MEVFQTD SHYIFVKRDKSLWWHRRTSEFSIKAGWDLSSVDDIECIGVTHGIVGVISLPNV 60
ME+FQ HYI + +++LW RR ++ DL + C+G+ G++G I L +
Sbjct: 1 MELFQAKDHYILOQGERALWCSRRDGGQLR PATDLLAWN PICLGLVEGVIGIKIQLHSD 60

Query: 61 YEPHLVVVKEASAVGVLYPPHLVYKIKSICILSADD---PD TDL PNCTKHTKSNQSTPTH 117
L+++++ + VG L H V K+ I +LS + D +L C KH
Sbjct: 61 LPWWLILIRQKALVGKLP GDHEVCKVT KIAVL SLSEMEPQDLELELCKKH----- 110

Query: 118 SVSTSNNNNASVPSSGGGSSKSTKLFEGMNKTWGAVKSAGNT---IKNTTQQAANLATKQ 174
G+NK + S ++ +K T +N++
Sbjct: 111 -----HFGINKPEKIIPSPDDSKFLLKTFTHIKSNVSAPN 145

Query: 175 VKSSVGIREPRHIERRITEELHKIFDETD SFYFSFDCDITNNLQRHEAKSEESQ---SQP 231
K +E +ERR+ EEL K+F +++SFY+S D+TN++QR + + +
Sbjct: 146 KKKVKESKEKEKLEERRLLEELLKMFMDSESFYYSLT YDLTNSVQRQSTGERDGRPLWQKV 205

Query: 232 DERFFWNKHMIRDLINLNDKT---WILPIIQGF MQVENCVIG----- 270
D+RFFWNK+MI+DL + WI+P+IQGF+Q+E V+
Sbjct: 206 DDRFFWNKYMIQDLTEIGTPD VDFWIIPMIQGFVQIEELVVNYTESSDDEKSSPETPPQE 265

Query: 271 NEC-----FTLALVSRRSRHRAGTRYKRRGVDEKGN CANYVETE QILSFRHHQLSFTQ 323
+ C F +AL+SRRSRHRAG RYKRRGVD+ GN ANYVETE Q++ +H LSF Q
Sbjct: 266 STCVDDIHPRFLVALISR SRHRAGMRYKRRGV DKNGNVANYVETEQLIHVHNHTLSFVQ 325

Query: 324 VRGSVPIYWSQPGYKYRPPRLDRGVAETQQA FELHFTKELETYGRVCIVNLVEQSGKEK 383
RGSVP++WSQ GY+Y P PRLDR ET F HF ++L Y + I+NLV+Q+G+EK
Sbjct: 326 TRGSVPVFWSQVGYRYNPRPRLDRSEKETVAYFCAHFEEQLNIYKKQVIINLVDQAGREK 385

Query: 384 TIGDAYADHVIKLNNDR LIYVTFDFHDYCRGMR FENV SALIDAVGPEAGAMGFHWRDQRG 443
IGDAY V+ NN L YV+FDH++CRGM+FENV L DA+ M + W D+ G
Sbjct: 386 IIGDAYLKQVLLFNNSHLTYVS FDFHEHCRGMKFENVQTLTDAIYDIILDMKWCWVDEAG 445

Query: 444 MICNQKSVFRVNCMDCLDR TNVVQTAIGKAVLESQ LVKLGLSPPYTP IPEQLKSPFMVLW 503
+IC Q+ +FRVNCMDCLDR TNVVQ AI + V+E QL KLG+ PP P+P + + ++W
Sbjct: 446 VICKQEGIFRVNCMDCLDR TNVVQAALARV VMEQQLKKGVMPP EQPLPVKCNRIYQIMW 505

Query: 504 ANNGDIISRQYAGTNALKG DYTRTGERKISGMMKDG MNSANRYYLARFKDSYRQATIDLM 563
ANNGD ISRQYAGT ALKGD+TRTGERK++G+MKDG+NSANRYYL RFKD+YRQA IDLM
Sbjct: 506 ANNGDSISRQYAGTAALKGDFTRTGERKLAGVMKDG VNSANRYYLNRFKDAYRQAVIDLM 565

Query: 564 LGNQVSSESLSALGGQAGPD---ENDGTENAEQAKLLVEDCRRLLLGTAQYPVGAWGLID 620
G V+ + S + + + + + E L++ +LLL + G W LID
Sbjct: 566 QGIPVTEDLYSIFTKEKEHEALHKNQRSHQELISQLLQSYMKLLLPDDEKFHGGWALID 625

Query: 621 ADPSSGDINETEVD TILLLTDDCYIVA EYDSHLDKIVRFEKVQLTQVRLIELGMHQQT KI 680
DPS D +VD +LLL++ Y VA YD +DK+ +++++ L + IE+G + +
Sbjct: 626 CDP SLIDATHRDVDVLLLLSNSAYYVAYYDDEVDKVNQYQRLSLENLEKIEIG--PEPTL 683

Query: 681 FQGSAPAHLCRLNYSVDEQEGYFHMFRSANLRFFNNMAYVIKTQEEVAESMTSIVEMFR 740
 F P C+RL+Y E GYFH R A + +E+ +++ I EM +
 Sbjct: 684 F--GKPKFSCMRLHYRYKEASGYFHTLR-----AVMRNPEEDGKDTLQCIAEMLQ 731

Query: 741 IALDNAGNTEVRYITGGVLQRRKSKLPTLDV-----PRGMPRNLSESQLVQLSSKA 791
 I G+ I L+R+ SK P D+ +N S+ L+ K
 Sbjct: 732 ITKQAMGSD--LPIIEKKLERKSSK-PHEDIIGIRSQNQGSQAQGNFLMSKFSSSLNQKV 788

Query: 792 LSNMA----GQFSKLGQTFKKPQAHPPSSLAATMNPQVMRQDSEIESGQEAQKAVFTLGR 847
 + G KLG F KP+ + L + + + DS +E+ + V +
 Sbjct: 789 KQTKSNVNIGNLRKLG-NFTKPEMKVNFLKPNLKVNLWKS-DSSLETMENT--GVMDKVQ 844

Query: 848 KHRNSNSASSTDTDEHDNSLYEPEVDSDEIAMDKSNYNE-NAFLPSVGIVMG----NQK 902
 + + +S D+ D L + D D ++A + + LPS GI+ +
 Sbjct: 845 AESDGDMSDDNDSDYHSDEFLTNSKSDEDRQLANSLESVGPIDYVLPSCGIIASAPRLGSR 904

Query: 903 EDSPSSSDEIRH 914
 S SS+D H
 Sbjct: 905 SQSLSSTDSSVH 916

Figure 4. Expression of the CG7956 Homologs in Mammalian Tissues

Figure 4A. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in wild type mouse tissues

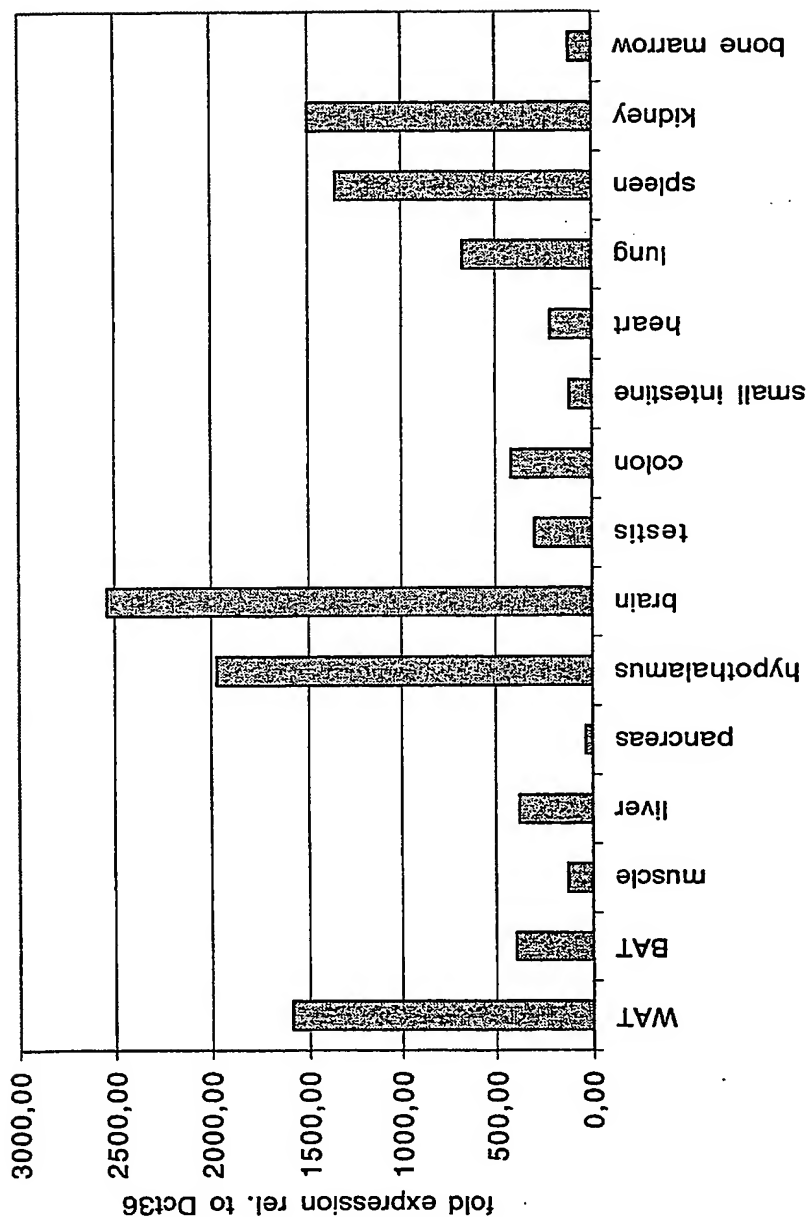


Figure 4B. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in different mouse models

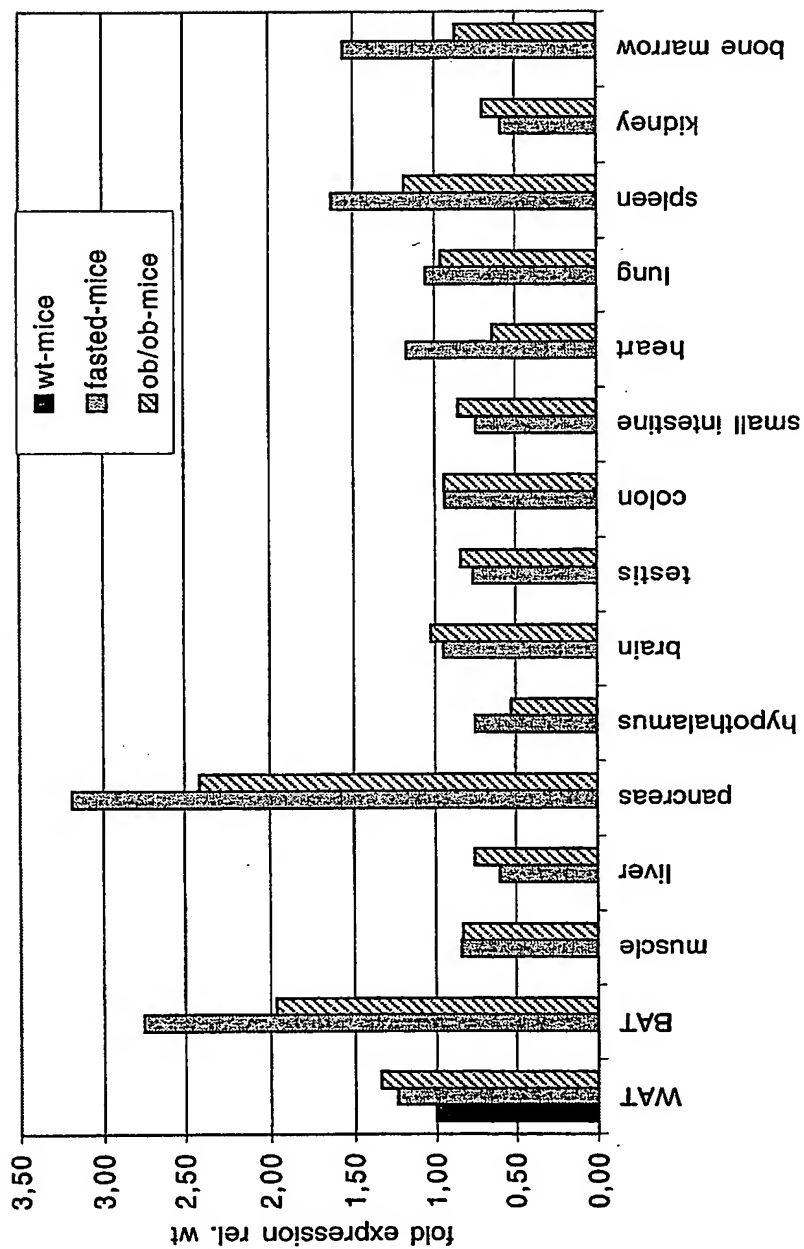


Figure 5. Triglyceride content of a *Drosophila aralar 1* (GadFly Accession Number CG2139) mutant

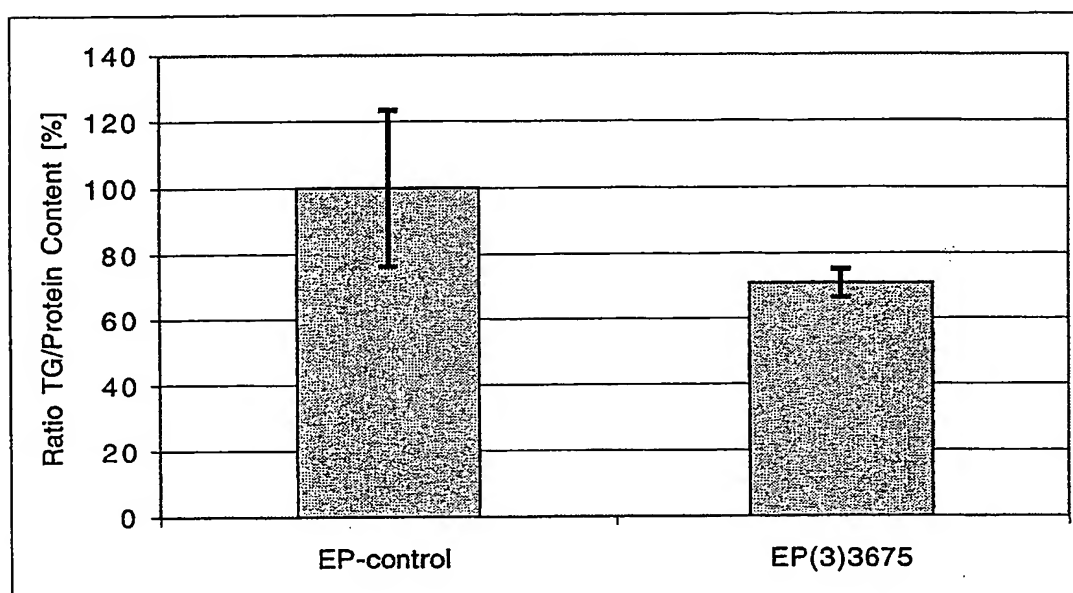


Figure 6. Molecular organisation of the *aralar 1* gene (GadFly Accession Number CG2139)

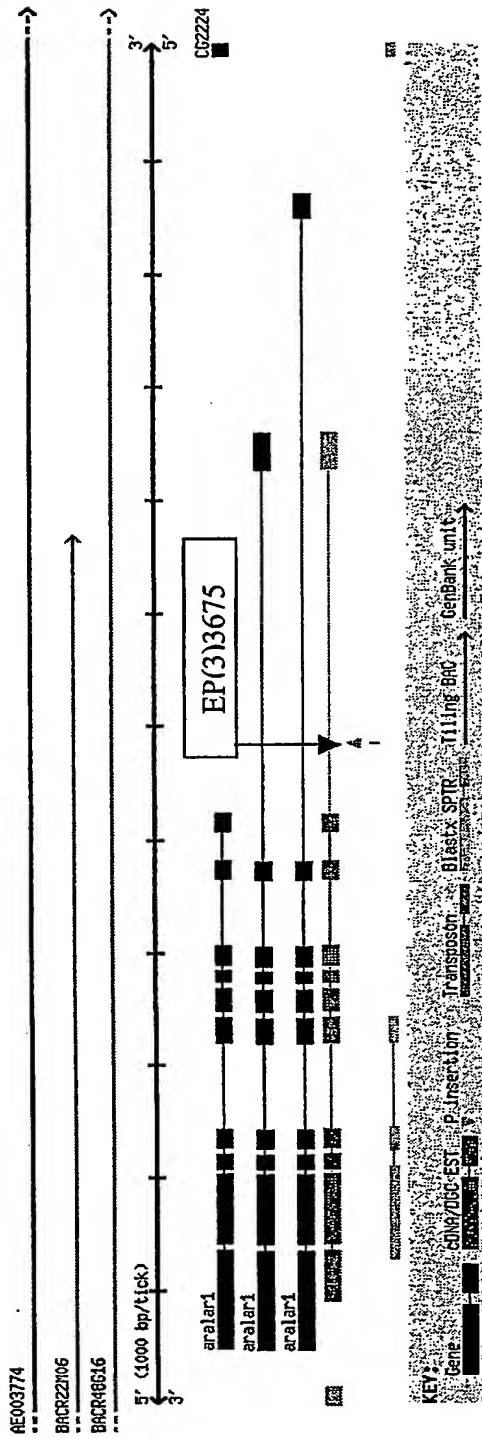


Figure 7. Homology of *Drosophila aralar 1* (GadFly Accession Number CG2139) to human solute carrier family 25, members 12 and 13

**Figure 7A. BLASTP results for *alarar 1*
Homology to human protein XP_010876.3 (GenBank Accession Number)**

ref|XP_010876.3| (XM_010876) solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Homo sapiens]
Length = 678

Score = 741 bits (1913), Expect = 0.0

Identities = 382/650 (58%), Positives = 488/650 (74%), Gaps = 14/650 (2%)

```

Query: 1   MTSEDFVRKFLGLFSESAFNDESVRLLANIADTSKDGILISFSEFQAFEGLLCTPDALYRT 60
          MT EDFV+++LGL+++   N + V+LLA +AD +KDGLIS+ EF AFE +LC PD+++
Sbjct: 34  MTPEDFVQRYLGLYNDPNSNPKIVQLLAGVADQTKDGLISYQEFALAFESVLCAPDSMFIV 93

Query: 61  AFQLFDRKNGTVSYADFADVQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
          AFQLFD+ GNG V++ + ++ +T +H IPF+ D FI+ +FG +++ +NY EFTQ
Sbjct: 94  AFQLFDKSGNGEVTFENVKEIFGQTIHHHIPFNWDCEFIRLHFGHNRRKHLNLTETQF 153

Query: 121 L HDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLLTPGVRDNLVSVTEG---HK 177
          L + EHA +AF KD + +G IS LDF DI+V ++ H+LTP V +NLVS G H+
Sbjct: 154 LQELQLEHARQAFALKDKSKSGMISGLDFSDIMVTIRSHMLTPFVEENLVSAAAGGSISHQ 213

Query: 178 VSFPHYFIATSLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQTMSQITPLEIDILF 236
          VSF YF AF SLLNNMEL++++Y G+R D+ +TK++ +A Q+TPLEIDIL+
Sbjct: 214 VSFSYFNAFNSLLNNMELVRKIY-STLAGTRKDVEVTKEEFAQSAIRYGQVTPLEIDILY 272

Query: 237 HLAGAVHQAGRIDYSDLSNIAPEHYTKHMTHLAEIKAVESPA-DRSAFIQVLESSYRFT 295
          LA + +GR+ +D+ IAP + + LAE++ +SP R ++Q+ ES+YRFT
Sbjct: 273 QLADLYNASGRLTLADIERIAPLAEGA-LPYNLAE LQRQQSPGLGRPIWLQIAESAYRFT 331

Query: 296 LGSFAGAVGATVVYPIDLVKTRMQNQR-AGSYIGEVA YRNSWDCFKKVVRHEGFMGLYRG 354
          LGS AGAVGAT VYPIDLVKTRMQNQR +GS +GE+ Y+NS+DCFKKV+R+EGF GLYRG
Sbjct: 332 LGSVAGAVGATAVYPIDLVKTRMQNQRGSGSVGELMYKNSFDCFKKVLRYEGFFGLYRG 391

Query: 355 LLPQLMGVAPEKAIKLTVNDLVRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEIVK 414
          L+PQL+GVAPEKAIKLTVND VRDK T + G++P AEVLAGGCAG SQV+FTNPLEIVK
Sbjct: 392 LIPQLIGVAPEKAIKLTVNDFVRDKFTRRDGSPVLP AEVLAGGCAGGSQVIFTNPLEIVK 451

Query: 415 IRLQVAGEIASGSKIRAWSVVRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMMAD 474
          IRLQVAGEI +G ++ A +V+R+LG+FGLYKGA+AC LRD+PFSAIYFP YAH K ++AD
Sbjct: 452 IRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLLLAD 511

Query: 475 KDGYNHPLTLAAGAIAGVPAASLVTPADVIKTRLQVVARSGQTTYTGVDATKKIMAE 534
          ++G+ L LLAAGA+AGVPAASLVTPADVIKTRLQV AR+GQTTY+GV D +KI+ EE
Sbjct: 512 ENGHVGGNLNLLAAGAMAGVPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILREE 571

Query: 535 GPRAFVKGTAAARVFRSSPQFGVTLVTYELLQRLFYVDFGGTQPKGSEAHKITTPLEQAAA 594
          GP AFWKGTAAARVFRSSPQFGVTLVTYELLQR FY+DFGG +P GSE TP + A
Sbjct: 572 GPSAFWKGTAAARVFRSSPQFGVTLVTYELLQRWFYIDFGGLKPAGSE----PTP-KSRIA 626

Query: 595 SVTTENVDHIGGYRAAVPLLAVESKFGLYLPRF-GRGVTAASPSTATGS 643
          + N DHIGGYR A AG+E+KFGLYLP+F V P A +
Sbjct: 627 DLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSAVAVVQPKAAVAA 676

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Homology to human protein NP_055066.1 (GenBank Accession Number)

ref|NP_055066.1| (NM_014251) solute carrier family 25, member 13 (citrin)
[Homo sapiens]
Length = 675

Score = 728 bits (1878), Expect = 0.0
Identities = 374/643 (58%), Positives = 476/643 (73%), Gaps = 17/643 (2%)

Query: 1 MTSEDFVRKFLGLFSESASFNDSESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRT 60
M+ DFV ++L +F ES N ++V LL+ + D +KDGLISF EF AFE +LC PDAL+
Sbjct: 35 MSPNDFVTRYLNIFGESQPNPKTVELLSGVVDQTKDGLISFQEFVAFESVLCAPDALFMV 94

Query: 61 AFQLFDRKNGTVSYADFADVVQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
AFQLFD+ G G V++ D V +T +H IPF+ D F++ +FG +++R + YAEFTQ
Sbjct: 95 AFQLFDKAGKGEVTFEDVKQVFGQTTIHQHIFPNWDSEFVQLHFGKERKRHLTYAEFTQF 154

Query: 121 LHDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLTPGVRDNLVSVTEG---HK 177
L + EHA +AF +D A TG ++ +DF+DI+V ++ H+LTP V + LV+ G H+
Sbjct: 155 LLEIQLEHAKQAFVQRDNARTGRVTAIDFRDIMVTIRPHVLTPEVEECLVAAAGGTTSHQ 214

Query: 178 VSFPYFIAFTSLLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQTMSQITPLEIDILF 236
VSF YF F SLLNNMELI+++Y G+R D+ +TK++ +LAAQ Q+TP+E+DILF
Sbjct: 215 VSFSYFNGFNSSLNNMELIRKIY-STLAGTRKDVEVTKEEFVLAAQKFGQVTPMEVDILF 273

Query: 237 HLAGAVHQAGRIDYSDLSNIAP-EHYTKHMTHLAEIKAVESPAD--RSAFIQVLESSYR 293
LA GR+ +D+ IAP E T + LAE + ++ D R +QV ES+YR
Sbjct: 274 QLADLYEPRGRMTLADIERIAPLEEGT--LPFNLAEAQRQKASGDSARPVLLQVAESAYR 331

Query: 294 FTLGSFAGAVGATVVYPIDLVKTRMQNQRA-GSYIGEYAYRNSWDCFKKVVRHEGFMGLY 352
F LGS AGAVGAT VYPIDLVKTRMQNQOR+ GS++GE+ Y+NS+DCFKKV+R+EGF GLY
Sbjct: 332 FGLGSVAGAVGATAVYPIDLVKTRMQNQORSTGSFVGELMYKNSFDCFKKVLRYEFGFGLY 391

Query: 353 RGLLPQLMGVAPEKAIKLTVNDLVDRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEI 412
RGLLPQL+GVAPEKAIKLTVND VRDK K G++P AE+LAGGCAG SQV+FTNPLEI
Sbjct: 392 RGLLPQLLGVAPEKAIKLTVNDLVDRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEI 451

Query: 413 VKIRLQVAGEIASGSKIRAWSVVRRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAM 472
VKIRLQVAGEI +G ++ A SVVR+LG FG+YKGA+AC LRD+PFSAIYFP YAH KA
Sbjct: 452 VKIRLQVAGEITTGPRVSALSVRDLGFFGIYKGAACFLRDIPFSAIYFPCYAHVKASF 511

Query: 473 ADKDGYNHPLTLAAGAIAGVPAASLVTPADVILKTRLQVVARSGQTTYTGVDATKKIMA 532
A++DG P +LL AGAIAG+PAASLVTPADVILKTRLQV AR+GQTTY+GV D +KI+
Sbjct: 512 ANEDGQVSPGSLLLAGAIAGMPAASLVTPADVILKTRLQVAARAGQTTYSGLVIDCFRKILR 571

Query: 533 EEGPRAFVKGTAAARVFRSSPQFGVTLVITYELLQRLFYVDFGGTQPKGSEAHKITTPLEQA 592
EEGP+A WKG ARVFRSSPQFGVTL+TYELLQR FY+DFGG +P GSE P+ ++
Sbjct: 572 EEGPKALWKGAGARVFRSSPQFGVTLTYELLQRFYIDFGGVKPMGSE-----PVPKS 625

Query: 593 AASVTTENVDHIGGYRAAVPLLAGVESKFGLYLPFRFGRGVTA 635
++ N DH+GGY+ AV AG+E+KFGLYLP F V+ +
Sbjct: 626 RINLPAPNPDHVGKYKLAVATFAGIENKFGLYLPFLFKPSVSTS 668

Figure 7B. Multiple Sequence Alignment (ClustalW 1.83)

```

aralar1 Dm  MPLTKSLPNSPSLLKRAGTEKLREVFLKYASIQKNGEHYMTSEDFVRKFLGLFSESASFND
SLC25A12 Hs  -----MAVKVQTTKRGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSNP
SLC25A13 Hs  -----MAAAKVALTKRADPAELRTIFLKYASIEKNGEFFMSPNDFVTRYLNIFGESQPNP

aralar1 Dm  ESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRTAFQLFDRKNGTQVSYADFADV
SLC25A12 Hs  KIVQLLAGVADQTKDGLISYQEFELAFESVLCAPDSMFIVAFQLFDKSGNGEVTFFENVKEI
SLC25A13 Hs  KTVELLSGVVDQTKDGLISFQEFVAFESVLCAPDALFMVAFQLFDKAGKGEVTFEDVKQV

aralar1 Dm  VQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQLLHDFHEEHAMEAFRSKDPAGT
SLC25A12 Hs  FGQTIHHHIPFNWDCEFIRLHFHGNRKKHLNYTEFTQFLQELQLEHARQAFALKDKSKS
SLC25A13 Hs  FGQTTIHQHIPFNWDSEFVQLHFGKERKRHLTYAEFTQFLLEIQLEHAKQAFVQRDNART

aralar1 Dm  GFISPLDFQDIIIVNVRHLLTPGVRDNLVSVTEG---HKVSFPYFIAFTSLLNNMELIKQ
SLC25A12 Hs  GMISGLDFSDIMVTIRSHMLTPFVEENLVSAAGGSIHQVSFSYFNAFNSLLNNMELVRK
SLC25A13 Hs  GRVTAIDFRDIMVTIRPHVLTFFVEECLVAAAGGTTSHQVSFSYFNGFNSLLNNMELIRK

aralar1 Dm  VYLHATEGSRTDMITKDQILLAAQMSQITPLEIDILFHLGAVHQAGRIDYSDLNIAPI
SLC25A12 Hs  IYSTLAGTRKDVEVTKEEFAQSAIRYQGVTPLEIDILYQLADLYNASGRLTLADIERIAPI
SLC25A13 Hs  IYSTLAGTRKDVEVTKEEFVLAQAQKFGQVTPMEVDILFQLADLYEPRGRMTLADIERIAPI

aralar1 Dm  EHYTKHMTHRLAEIKAVESPA--DRSAFIQVLESSYRFTLGSGFAGAVGATVVYPIDLVKT
SLC25A12 Hs  LAEG-ALPYNLAELQRQQSPG-LGRPIWLQIAESAYRFTLGSGVAGAVGATAVYPIDLVKT
SLC25A13 Hs  LEEG-TLPFNLAEAQRQKASGDSARPVLLQVAESAYRFGSGVAGAVGATAVYPIDLVKT

aralar1 Dm  RMQNQR-AGSYIGEVAYRNSWDCFKKVRHEGFMGLYRGLLPQLMGVAPEKAIKLTVNDL
SLC25A12 Hs  RMQNQRGSGSVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAIKLTVNDL
SLC25A13 Hs  RMQNQRSTGSGFVGELMYKNSFDCFKKVLRYEGFFGLYRGLLPQLLGVAPEKAIKLTVNDL

aralar1 Dm  VRDKLTDKKGNIPTWAEVLAGGCAGASQVVFTNPLEIVKIRLQVAGEIASGSKIRASVSV
SLC25A12 Hs  VRDKFTRRDGSSVPLPAEVLAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALNVL
SLC25A13 Hs  VRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALS SVV

aralar1 Dm  RELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMMADKDGYNHPLTLAAGAIAGVPA
SLC25A12 Hs  RDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLLADENGHVGGNLLAAGAMAGVPA
SLC25A13 Hs  RDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPA

aralar1 Dm  ASLVTPADVIRLQVVARSGQTTYTGVDATKKIMAEEGPRAFWKGTAAARVFRSSPQFG
SLC25A12 Hs  ASLVTPADVIRLQVAARAGQTTYSGVIDCFRKILREEGPSAFWKGTAAARVFRSSPQFG
SLC25A13 Hs  ASLVTPADVIRLQVAARAGQTTYSGVIDCFRKILREEGPKALWKAGARVFRSSPQFG

aralar1 Dm  VTLVTYELLQRLFYVDGGTQPKGSEAHKITTPLEQAAASVTTENVDHIGGYRAAVPLLA
SLC25A12 Hs  VTLVTYELLQRWFIYDFGGLKPKGSEP----TPKSRIAD-LPPANPDHIGGYRLATATFA
SLC25A13 Hs  VTLLTYELLQRWFIYDFGGVKPMGSEP----VPKSRIN--LPAPNPDHVGGYKLAVATFA

aralar1 Dm  GVESKFGLYLPRFGRGVTAASPSTATGS---
SLC25A12 Hs  GIENKFGLYLPKFKSPSAVVQPKAAVAATQ
SLC25A13 Hs  GIENKFGLYLPFLK-PSVSTSKAIGGGP---
```

Figure 8. Expression of *aralar 1* Homologs in Mammalian Tissues

Figure 8A. Real-time PCR analysis of Slc25a12 expression in wild type mouse tissues (DCt Pancreas = 18,94)

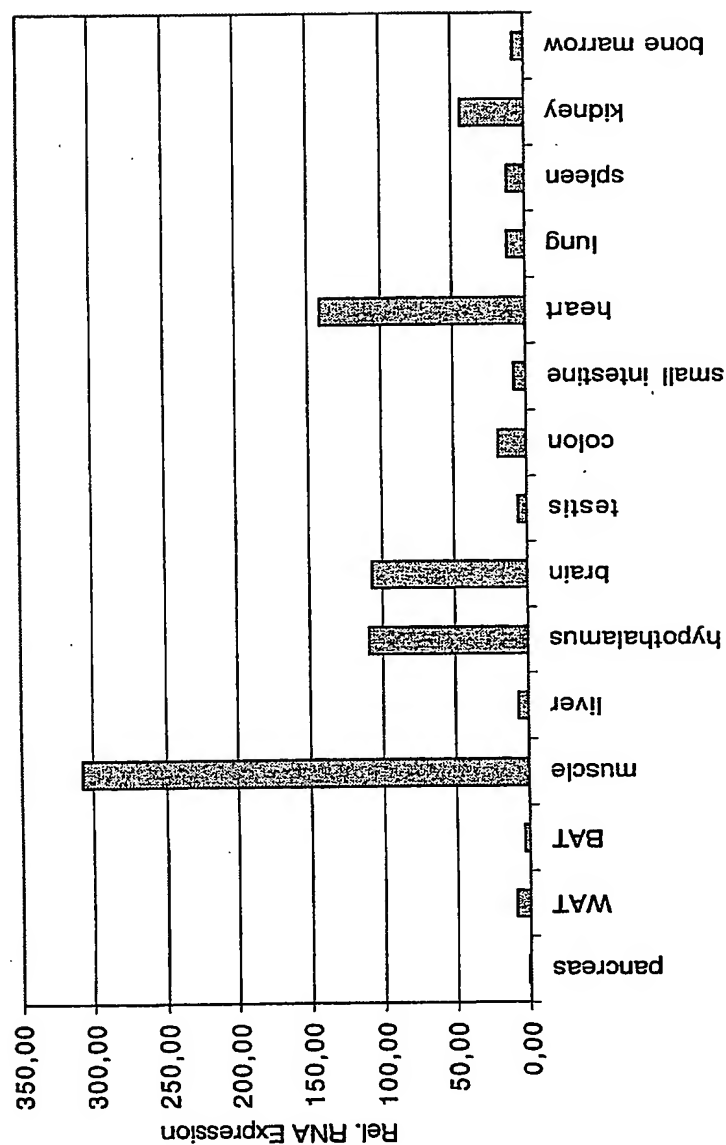


Figure 8B. Real-time PCR analysis of Slc25a12 expression in different mouse models

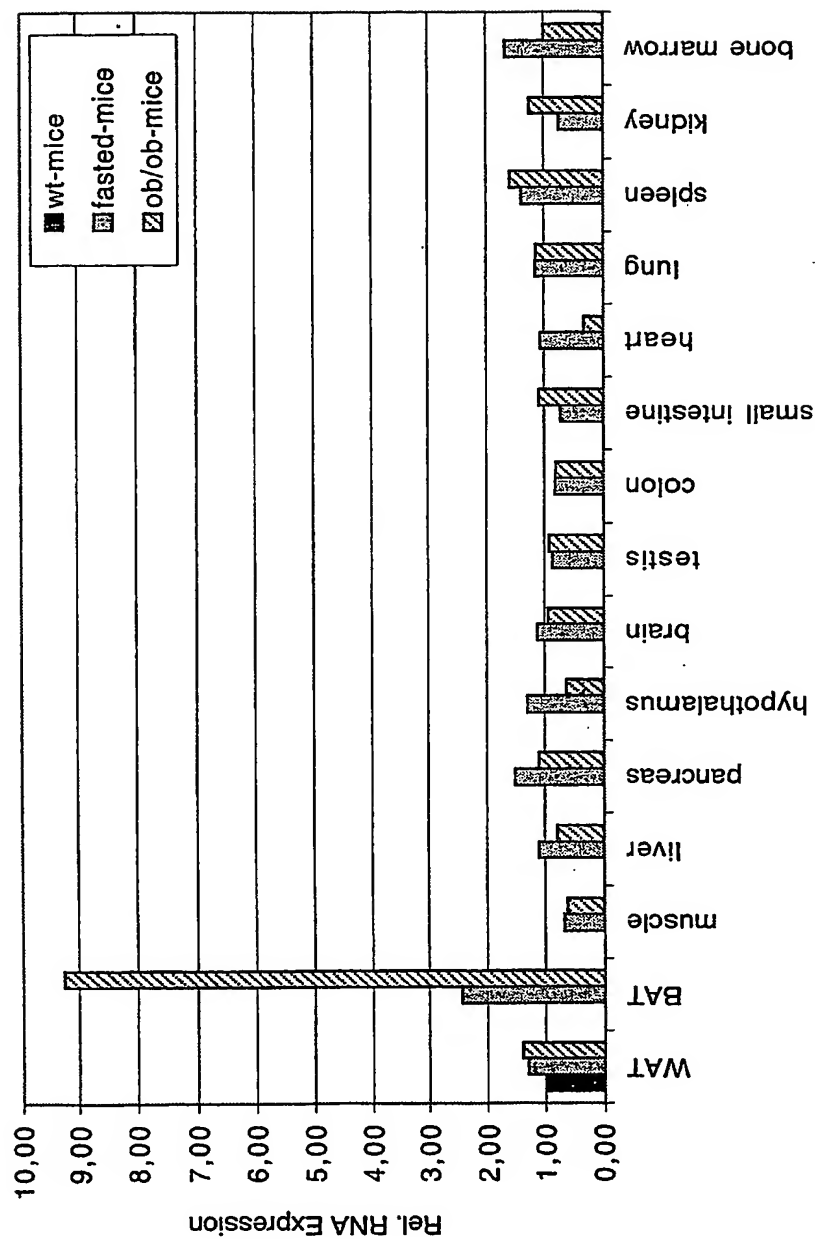


Figure 8C. Real-time PCR analysis of Slc25a13 expression in wild type mouse tissues (DCt Pancreas = 20,41)

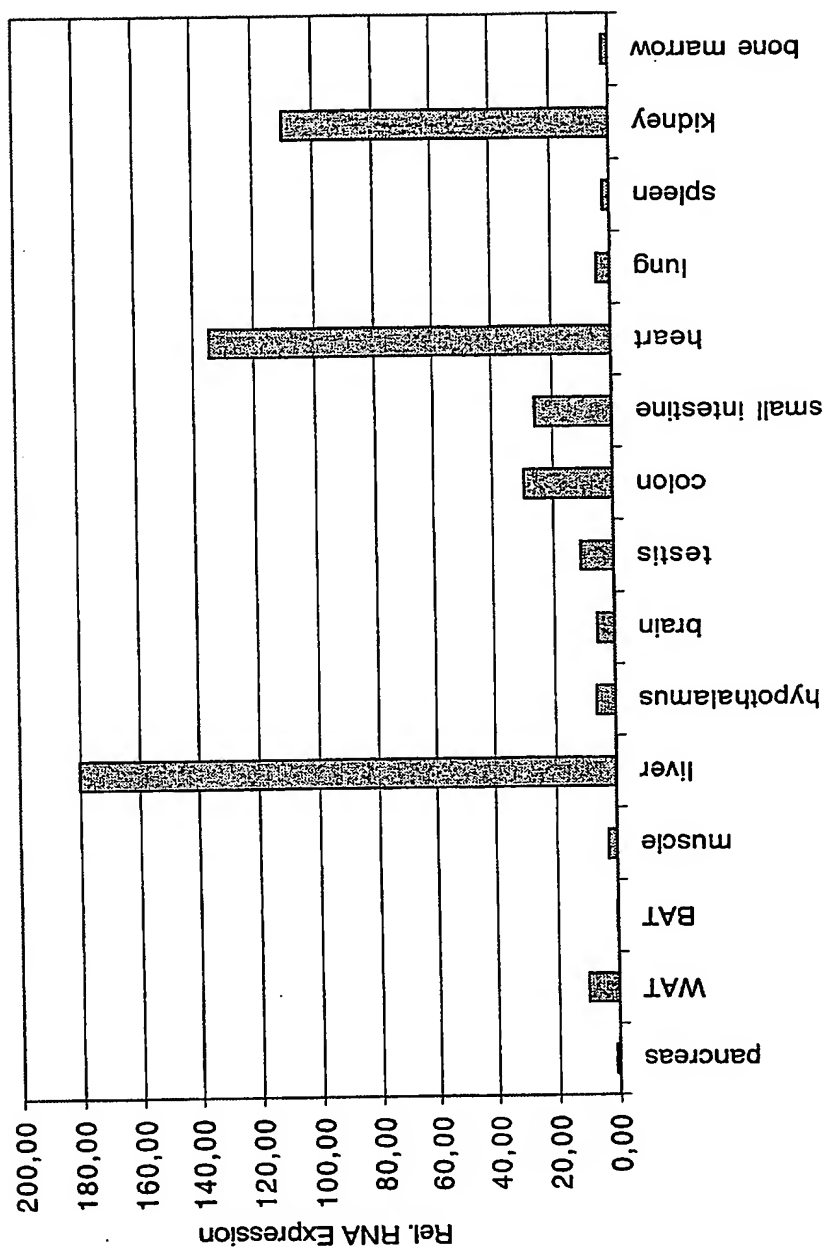


Figure 8D. Real-time PCR analysis of Slc25a13 expression in in different mouse models

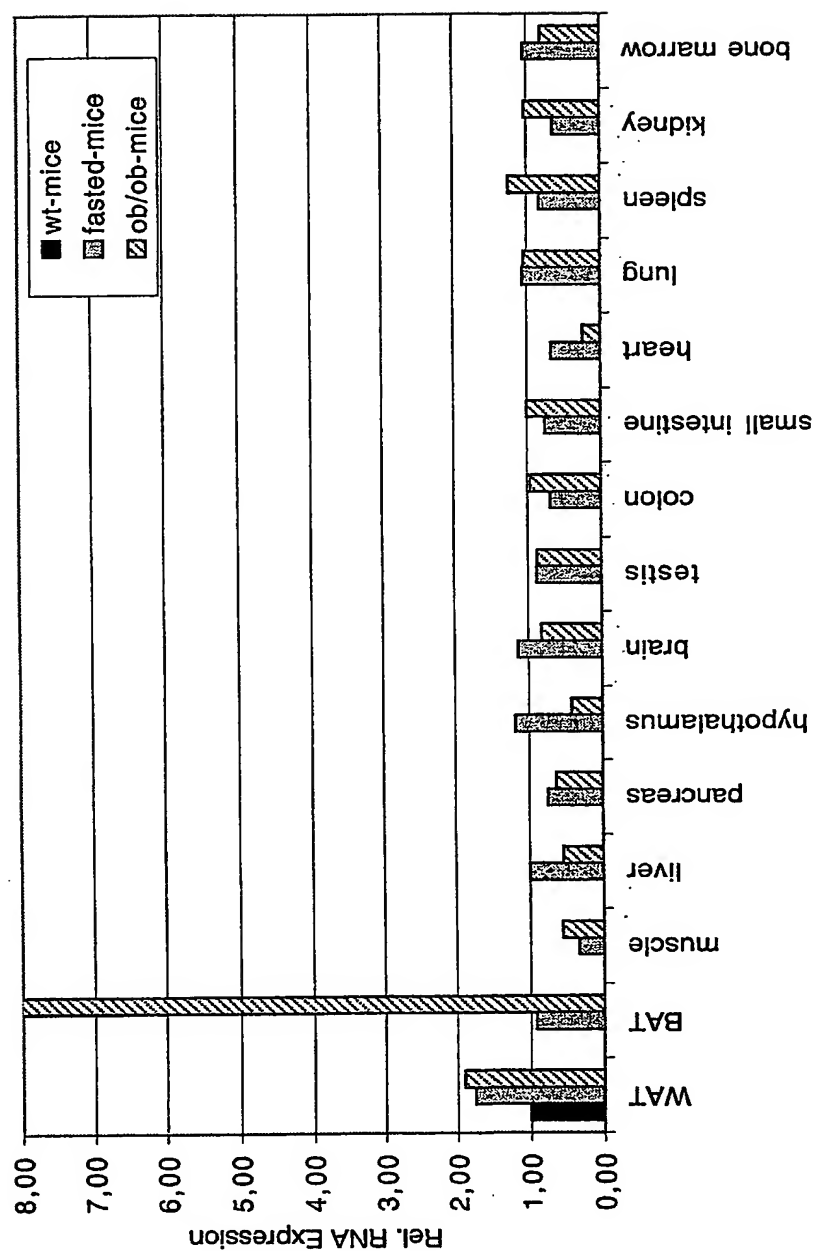


Figure 9. Triglyceride content of a *Drosophila how* (GadFly Accession Number CG10293) mutant

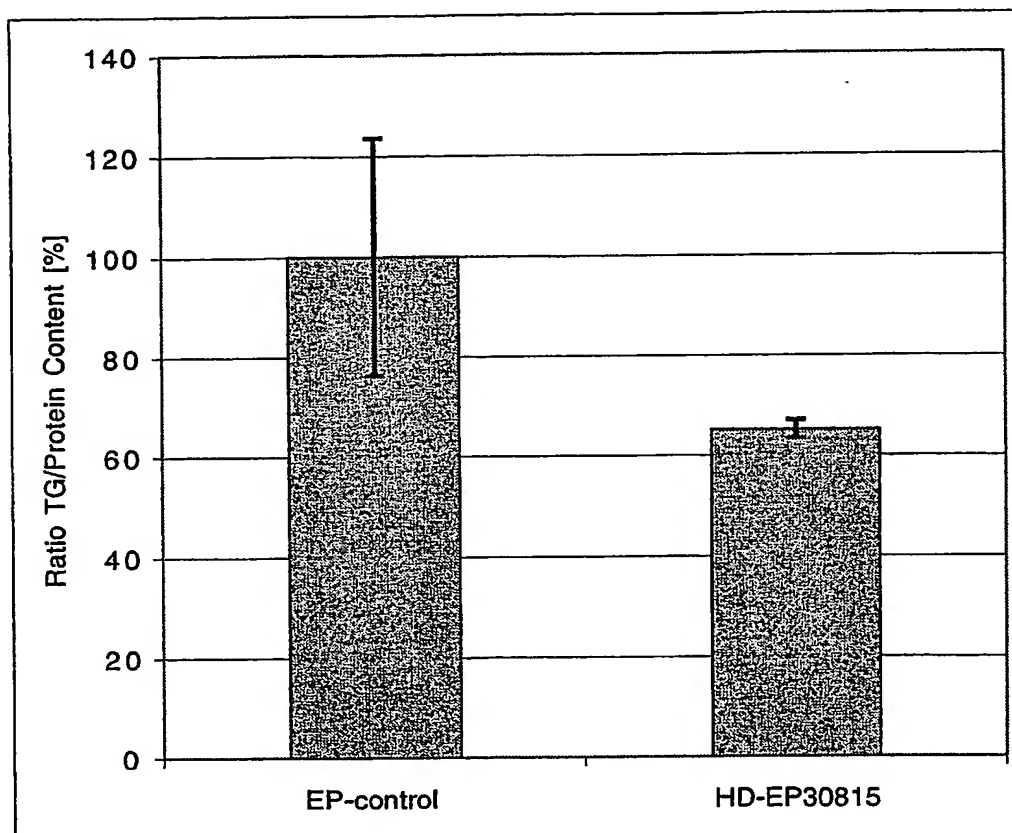


Figure 10. Molecular organisation of the *how* gene (GadFly Accession Number CG10293)

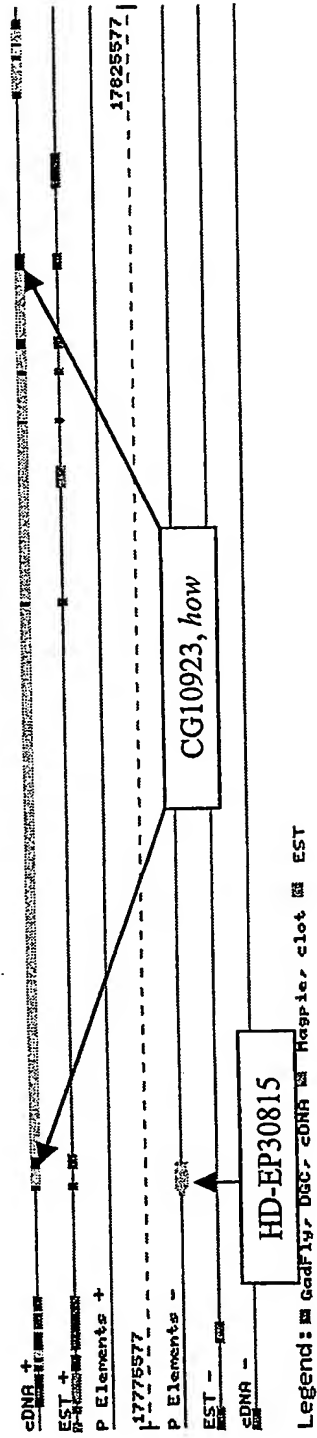


Figure 11. Homology of *Drosophila how* (GadFly Accession Number CG10293) to human Quaking isoforms

Figure 11A. BLASTP results for CG10293 (GadFly Accession Number)

gb|AAF63416.1|AF142421_1 (AF142421) QUAKING isoform 5 [Homo sapiens]
Length = 337

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDCLKKMLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIIVPPGPEAGLIYTPYEYP-YTLAP 292

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 293 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 326

ref|XP_037438.2| (XM_037438) similar to KH domain RNA binding protein QKI-5A
[Homo sapiens], Length = 341

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDCLKKMLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

19/51

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIIVPPGPEAGLIYTPYEYP-YTLAP 296

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 297 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 330

gb|AAF63414.1|AF142419_1 (AF142419) QUAKING isoform 6 [Homo sapiens]
Length = 363

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPNN--VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 88 EKRSAELPDVAGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIIVPPGPEAGLIYTPYEYP-YTLAP 318

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 319 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 352

dbj|BAB55032.1| (AK027309) unnamed protein product [Homo sapiens]
Length = 323

Score = 282 bits (722), Expect = 5e-75
Identities = 165/320 (51%), Positives = 208/320 (64%), Gaps = 20/320 (6%)

Query: 81 QLLKDRKQLAAFPNN--VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEPEGSV 134
QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+ G +
Sbjct: 2 QLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGSTEKRSAELPDVAGPI 61

Query: 135 VTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKEDANR 194
V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE+ NR
Sbjct: 62 VQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKEQNR 121

Query: 195 GKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPAEGEDELKKRQLMELAI 254
GKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLMELAI
Sbjct: 122 GKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAEAGEDSLKKMQLMELAI 181

Query: 255 INGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAPLILN 313
+NGTYRD KS A+ A + R++T A +R P A P PLI
Sbjct: 182 LNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRTPTPAGPTIMPLIRQ 239

Query: 314 PRMTVPPTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYADHS-- 369
+ V + + PTAA G G+I+ PY+Y Y +L + S
Sbjct: 240 IQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIEPSGV 292

Query: 370 VGAIKQORRLATNREHPYQR 389
+GA+ + R R HPYQR
Sbjct: 293 LGAVATKVRRHDMRVHPYQR 312

gb|AAF63413.1|AF142418_1 (AF142418) QUAKING isoform 2 [Homo sapiens]
Length = 347

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKMDYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPPTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63417.1|AF142422_1 (AF142422) QUAKING isoform 3 [Homo sapiens]
Length = 341

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKMDYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 266 PTPAGPTIMPLIRIQITAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63415.1|AF142420_1 (AF142420) QUAKING isoform 4 [Homo sapiens]
Length = 315

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEQNKGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 240 PTPAGPTIMPLIRIQITAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BAB69497.1| (AB067799) RNA binding protein HQK-6 [Homo sapiens]
Length = 319

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKEQNKGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69499.1| (AB067801) RNA binding protein HQK-7B [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKMLSSLPNFCGIFNHLERLLDEEISVRKMDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69498.1| (AB067800) RNA binding protein HQK-7 [Homo sapiens]
 Length = 325

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKMLSSLPNFCGIFNHLERLLDEEISVRKMDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

gb|AAF63412.1|AF142417_1 (AF142417) QUAKING isoform 1 [Homo sapiens]
Length = 321

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDVGPVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDCLKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BD004960.1| Genes related to stomach cancer, Length = 1993

Score = 288 bits (738), Expect = 1e-77
Identities = 168/324 (51%), Positives = 211/324 (64%), Gaps = 11/324 (3%)
Frame = +1

Query: 77 DYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEP 130
DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+
Sbjct: 4 DYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGSTEKRSaelPDA 183

Query: 131 EGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKE 190
G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE
Sbjct: 184 VGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKE 363

Query: 191 DANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEGEDELKKRQLM 250
+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLM
Sbjct: 364 EQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEGEDSLKMQLM 543

Query: 251 ELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAP 309
ELAI+NGTYRD KS A+ A + R++T A +R P A P P
Sbjct: 544 ELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRTPTPAGPTIMP 717

Query: 310 LILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYAD 367
LI + V + + PTAA G G+I+ PY+Y Y +L +
Sbjct: 718 LIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY-PYTLAPATSILEYPIE 876

Query: 368 HS--VGAIKQORRLATNREHPYQR 389
S +GA+ + R R HPYQR
Sbjct: 877 PSGVLGAVATKVRHDMRVHPYQR

[illegible]

Figure 12. Expression of human *low* homologs in mammalian (human) tissue

Figure 12A. Quantitative analysis of Quaking 6 (QKI-6) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

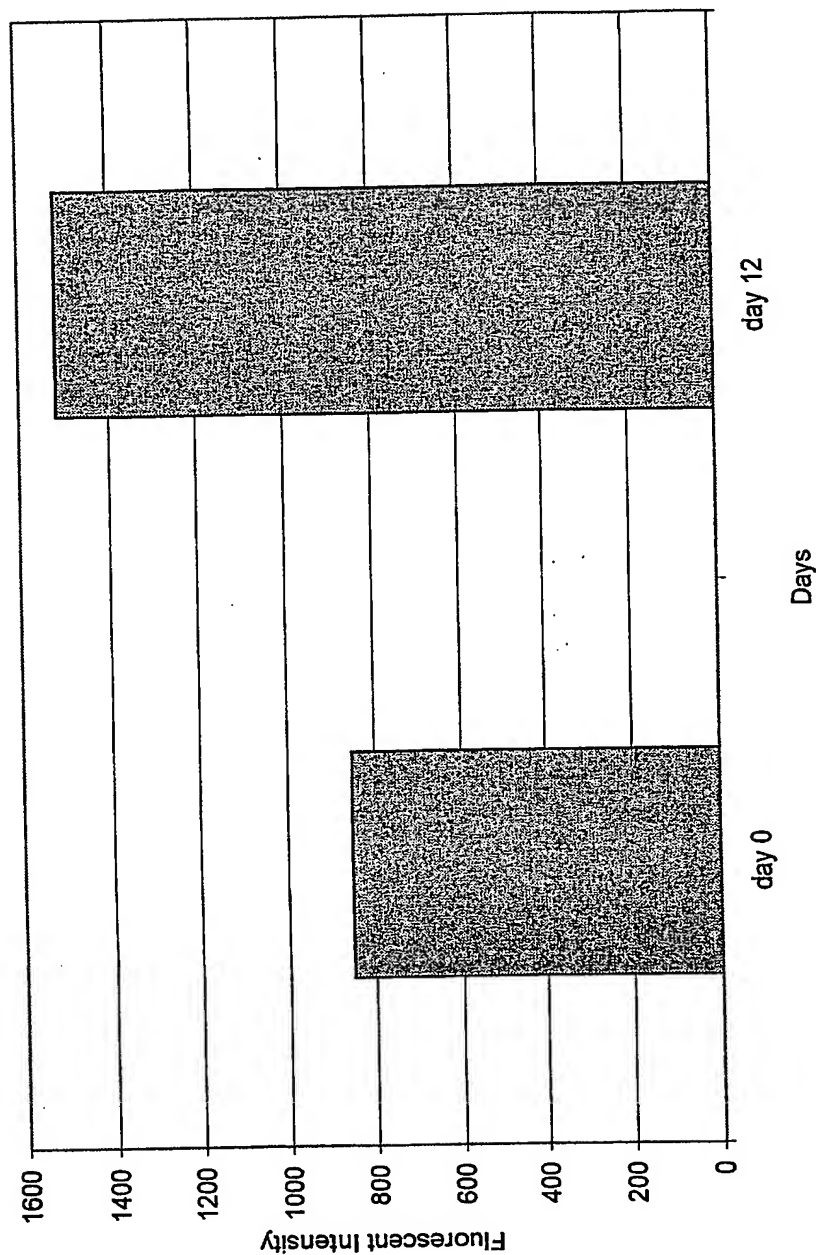


Figure 12B. Quantitative analysis of human RNA binding protein HQK-7B expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

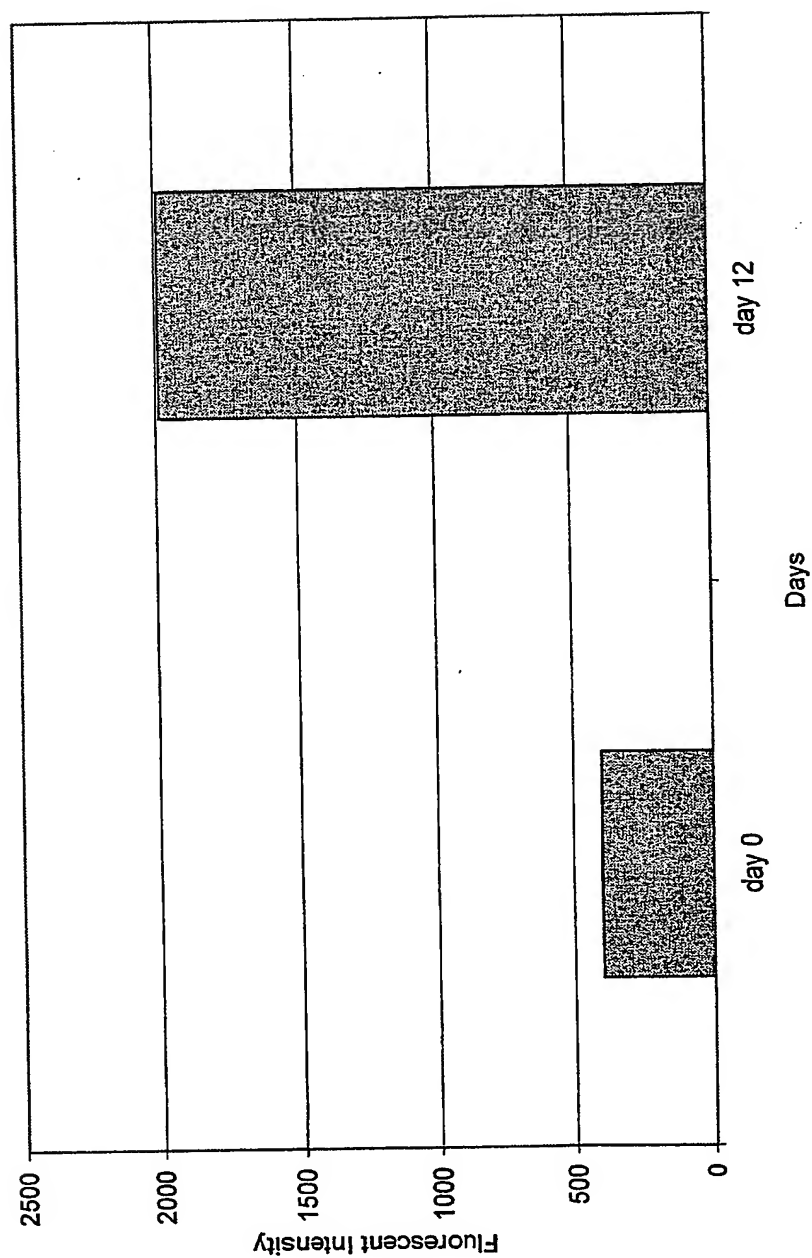


Figure 13. Triglyceride content of a *Drosophila* CG9373 (GadFly Accession Number) mutant

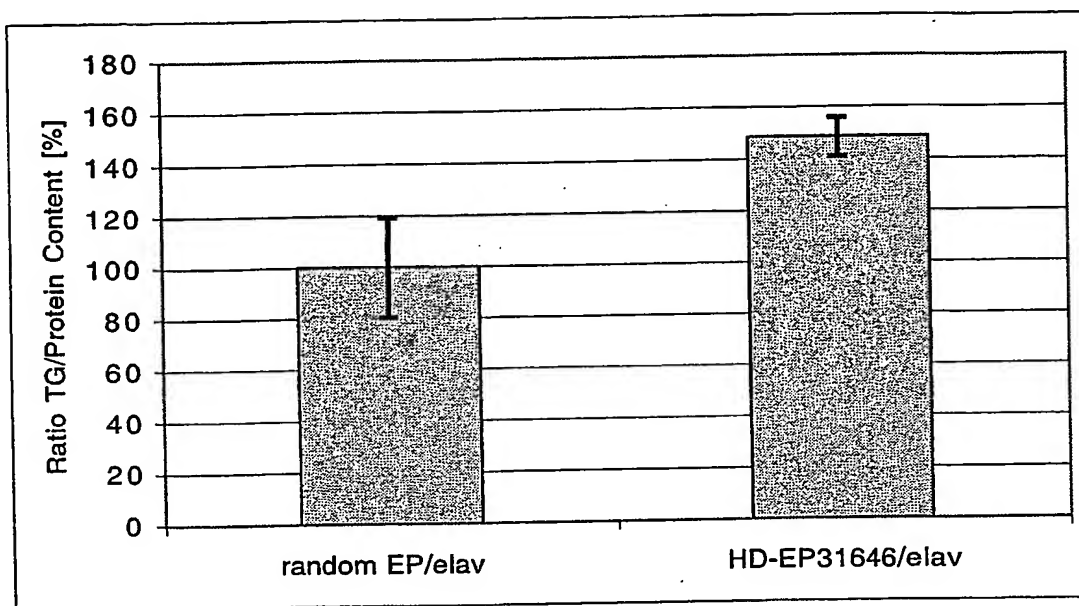


Figure 14. Molecular organisation of the CG9373 gene (GadFly Accession Number)

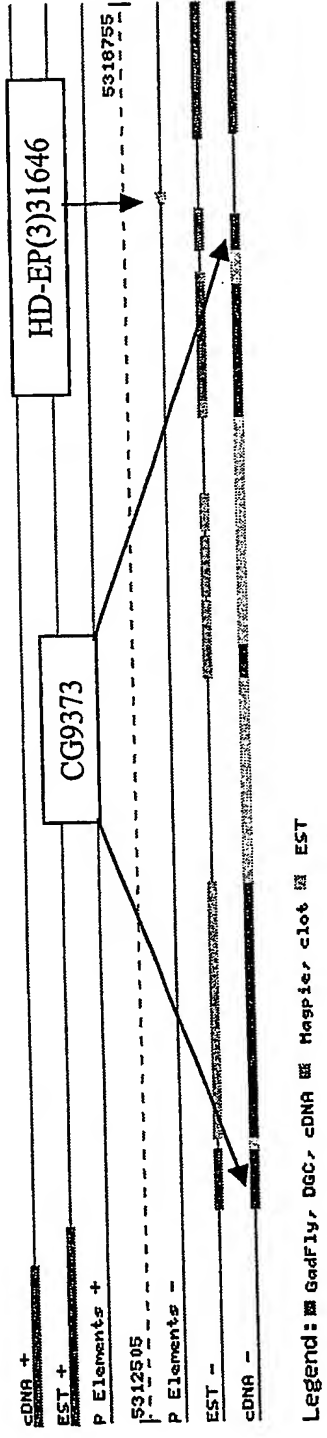


Figure 15. Homology of Drosopila GadFly Accession Number CG9373 to human KIAA1443 protein, human unnamed protein product, and human myelin gene expression factor 2

**Figure 15A. BLASTP results for GadFly Accession Number CG9373
Homology to human protein BAA92579.1 (GenBank Accession Number)**

dbj|BAA92579.1| (AB037762) KIAA1341 protein [Homo sapiens], Length = 620

Score = 249 bits (635), Expect = 1e-64
Identities = 207/660 (31%), Positives = 295/660 (44%), Gaps = 148/660 (22%)

```

Query: 1  MSMDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
      + M+  S + + + + G++ +RF      + N G G + G      RN R
Sbjct: 72  VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 121

Query: 59  VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
      V+ISNIPYD +WQ +KDL R  VG + YV+LF D  GK+RCCG+VEFKD E V+KALE M
Sbjct: 122 VFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 181

Query: 119  NRYEVNGRELVVKEDHGEQORDQYGRIVRDGGGGGGGGGGVQGGNGGNGGGGGGGGRDHMD 178
      N+Y+++GR L +KED  + + + R GG  GG      H+
Sbjct: 182 NKYDLSGRPLNIKEDPDGENARRA-LQRTGGSFPGG-----HVP 219

Query: 179  DRDRGFSSRRDDRLSGRNNFNMMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKV FVAN 238
      D  G      L  NN N+  +N      +G L + +FVAN
Sbjct: 220 DMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVAN 259

Query: 239  LDYKVDNKKLKQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLF 298
      LD+KV  KKLK+VF +AG V+  D+  DK+G SRG  + ++  +EAVQAISM + Q LF
Sbjct: 260 LDFKVGWKKLKEVFSIAGTVKRADIKEDKD GKS RGMGTVTTFEQAI EAVQAISM FNQGQFLF 319

Query: 299  DRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQSQ 350
      DR M V++D  +P +      + +LP GLGG+G+GLGP G+P+  N+
Sbjct: 320 DRPMHVKMDDKSV PHEEYRSHDGKTPQLPRGLGGIGMGLPGGQPISASQLNI----- 372

Query: 351  GQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNLTGVMFGNHAAVQSPVAPVQKPSL 410
      G ++GN  G      + G  FG      +
Sbjct: 373 GGVMGNLGP GGM-----GMDGPGFGG-----MNRI 397

Query: 411  GNNTGSGGLN LNNLNPSILA AVVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGNS 462
      G  G GGL  N      +G G G G L  ++SS+      ++G+N G
Sbjct: 398 GGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRGFG 449

Query: 463  GNDDNLPPSNVGLSNNYSSGGTGGGNSYSSGNYSGGGGSSN-----LGYNAYSSS-G 514
      +  L + +G      +G G N  G+  SGG GS N      +G +  SSS
Sbjct: 450 DSFGRLGSAMIG----GFAGRIGSSNMGPVGSIGSGMGSMNSVTGGMGMLDRMSSSFD 505

Query: 515  GMGGGNGGVGV DGN DYNTGNPLDVYGGGNSVGN SNVGSANAVGASRKSDTIIKNVPITC 574
      MG G G +  D + G      G G      +GS      K + I ++N+P
Sbjct: 506 RMGP GIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDL 554

Query: 575  TWQTLRDKFREIGDVKFAEI-----RGNDVGVRFFKERDAELALMDGSRLDGRNIKV 629
      TWQ L++KF + G V FAEI      +  G VRF      AE A  +M+G ++ GR I V
Sbjct: 555 TWQKLKEKFSQCCHVMFAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 614

```

Score = 68.6 bits (166), Expect = 2e-10
Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +
Sbjct: 510 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 565

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELVVKED 133
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 566 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 617

Score = 56.2 bits (134), Expect = 1e-06
Identities = 46/180 (25%), Positives = 76/180 (41%), Gaps = 21/180 (11%)

Query: 139 DQYGRIVRDGGGGGGG-----GGGVQGGNGGNNGGGGGGRDHMDRDRGRFSRRD 188
D +GR+ GG G G G+ GG G N GG G +D F R
Sbjct: 450 DSFGRLGSAMIGGFAGRIGSSNMGPVSGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM- 507

Query: 189 DDRLSGRNNFNMSNDYNNSSNYNLYGLSASFLESIGISGPLHNKVFVANLDYKVDNKKL 248
G ++ + + + + E +G G N++FV NL + + +KL
Sbjct: 508 -----GPGIGAILERSIDMDRGFLSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKL 559

Query: 249 KQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
K+ F G V ++ ++ G S+G + +D P A +A +++ + R + VRLDR
Sbjct: 560 KEKFSQCGHVMFAEIKMEN-GKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 618

Homology to human protein BAB14421.1 (GenBank Accession Number)

>dbj|BAB14421.1| (AK023133) unnamed protein product [Homo sapiens],
Length = 576

Score = 242 bits (618), Expect = 1e-62
Identities = 206/654 (31%), Positives = 289/654 (43%), Gaps = 160/654 (24%)

Query: 1 MSMDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
+ M+ S + + + + G++ +RF + N G G + G RN R
Sbjct: 52 VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 101

Query: 59 VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
Sbjct: 102 VFISNIPYDMKWQAIDLMREKVGEVTVYELFKDAEGKSRGCGVVEFKDEEFVKKALETM 161

Query: 119 NRYEVNGRELVVKED-HGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGGRDHM 177
N+Y+++GR L +KED GE + + R GG GG H+
Sbjct: 162 NKYDLSGRPLNIKEDPDGENARRASQ--RTGGSFPGG-----HV 198

Query: 178 DDRDRGFSRRDDRLSGRNNFNMSNDYNNSSNYNLYGLSASFLESIGISGPLHNKVFVA 237
D G L NN N+ +N +G L + +FVA
Sbjct: 199 PDMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVA 238

Query: 238 NLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQML 297
NLD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q L
Sbjct: 239 NLDKFGVKKLKEVFSIAGTVKRAKIDKDKGSRGMGTVTFEQAIEAVQAISMFGQFL 298

Query: 298 FDRRMTVRLD--RIPDK-----NEGKLPGLGGVGIGLGPNGEPLRDVAHNLPNGGQS 349

FDR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+
 Sbjct: 299 FDRPMHVKMDDKSVPH EYRSHDGTKPQLPRGLGGIGMGLGPGGQPISASQLNI----- 352
 Query: 350 QGQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHAAVQSPVAPVQKPS 409
 G ++GN G + G FG
 Sbjct: 353 -GGVMGNLGP GGM-----GMDGPGFGG-----MNR 376
 Query: 410 LGNNTGSGGLNLMNLNPSILAAVVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGN 461
 +G G GGL N +G G G G L ++SS+ ++G+N G
 Sbjct: 377 IGGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRG- 427
 Query: 462 SGNDNLPPSNVGLSNNYSSGGTGGGNSYSSGNNYSGGGSSNLGYNAYSSS-GGMGGGN 520
 G S GG GG NS + G +G + SSS MG G
 Sbjct: 428 -----FGDSFGRLGGGMGGMNSVT-----GGMGMGLDRMSSSFDRMGPGI 467
 Query: 521 GGVGVDGNDYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTIIKKNVPITCTWQTLR 580
 G + D + G G G +GS K + I ++N+P TWQ L+
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLTWQKLK 516
 Query: 581 DKFREIGDVKFAEI-----RGNDVGVRFFKERDAELALALMDGSRLDGRNIKV 629
 +KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 517 EKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDV 570

Score = 72.8 bits (177), Expect = 1e-11
 Identities = 82/348 (23%), Positives = 133/348 (37%), Gaps = 96/348 (27%)

Query: 54 RRNCRVYISNIPYDWRQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQK 113
 R ++++N+ + W+ LK++F I G+++ + D+ GK+RG G V F+ +
 Sbjct: 230 RLGSTIFVANLDFKVGWKKLKEVFS-IAGTVKRADIKEDKD GKS RGMGTVTTFEQAI EAVQ 288
 Query: 114 ALEKMNRYEVNGREL VVKED-----HGEQRDQYGRIVRDGGGGGGGG----- 155
 A+ N + R + VK D H E R G+ + G GG G
 Sbjct: 289 AISMFNGQFLFDRPMHVKMDDKSVPH EYRSHDGTKPQLPRGLGGIGMGLGPGGQPISAS 348
 Query: 156 ----GGVQG-----GNGGNNGGGG-----GGRDHMDDRDRGF 184
 GGV G G GG N GGG GG M + RG
 Sbjct: 349 QLNIGGVMGNLGP GGMGMDGPGFGGMNRIGGGIGFGGLEAMNSMGGFGGVGRMGELYRGA 408
 Query: 185 SRRDDRLSGRNNFNMMS-----NDYNNSSNYNLYGLSASFLES LG--- 225
 +R GR + + N L +S+SF + +G
 Sbjct: 409 MTSSMERDFGRGDIGINRGFGDSFGRLGGGMGGMNSVTGGMGMGLDRMSSSF-DRMGPGI 467
 Query: 226 -----ISGPLH-----NKVFVANLDYKVDNKKLKQVFKLAGKVQS 260
 +SGP+ N++FV NL + + +KLK+ F G V
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGMRERIGSKGNQIFVRNLPFDLTWQKLKEKFSQCGHVMF 527
 Query: 261 VDLSLDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
 ++ ++ G S+G + +D P A +A +++ + R + VRLDR
 Sbjct: 528 AEIKMEN-GKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDR 574

Score = 68.6 bits (166), Expect = 2e-10
 Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDWRQDLKDLFRR 79
 G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +
 Sbjct: 466 GIGAILERSIDMD-RGFLSGPMGSGM---RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 521
 Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGREL VVKED 133

G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
 Sbjct: 522 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLD 573

Homology to human protein NP057216.1 (GenBank Accession Number)

ref|NP_057216.1| (NM_016132) myelin gene expression factor 2 [Homo sapiens]
 gb|AAD43038.1| (AF106685) myelin gene expression factor 2 [Homo sapiens]
 Length = 547

Score = 238 bits (607), Expect = 2e-61
 Identities = 204/659 (30%), Positives = 295/659 (43%), Gaps = 150/659 (22%)

Query: 3 MDASNSVESREKERDRRGRGAR-GSRFTDADGNNG-AGSQGGGVAARDRSRERRNCRVY 60
 M+ S + + + + G++ +RF + N G G + G RN RV+
 Sbjct: 1 MENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-RVF 50

Query: 61 ISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNR 120
 ISNIPYD +WQ +KDL R VG + YV+LF D GK+RCCG+VEFKD E V+KALE MN+
 Sbjct: 51 ISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRCCGVVEFKDEEFVKKALETMNK 110

Query: 121 YEVNGRELVVKEDHGEQORDQYGRIVRDGGGGGGGGGGVQGGNGGNGGGGGGGGRDHMDDR 180
 Y+++GR + +KED + + + R G QG + + G G
 Sbjct: 111 YDLSGRRVNIKEDPDGENARRA-LQRTGTS-----FQGS HASDVGSG----- 151

Query: 181 DRGFSRRDDRLSGRRNFMMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVANLD 240
 N+ + NN + + + +L + +L + +FVANLD
 Sbjct: 152 -----LVNLPSPILNNPN-----IPPEVISNLQ-AGRLGSTIFVANLD 188

Query: 241 YKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLFDR 300
 +KV KKLK+VF +AG V++ DK+G SRG + ++ +EAVQAISM + Q LFDR
 Sbjct: 189 FKVGWKKLKEVFSIAGTVKAGSYKEDKDGSRGMGTVTFEQAI EAVQAISM FNQQLFDR 248

Query: 301 RMTVRLD-----RIPDKNEGILPEGLGGVGIGLGPNGEPLRDVAHNL PGGQSQG 351
 M V++D R PD + +LP GLGG+G+GLGP G+P+ N+ G
 Sbjct: 249 PMHVKMDDKSPHEEYRSPD-GKTPQLPRGLGGIGMGLGPGGQPISASQLNI-----G 300

Query: 352 QLLGNAQQGSQSGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHA AVQSPVAPVQKPSLG 411
 ++GN G + G FG +G
 Sbjct: 301 GVMGNLGP GGM-----GMDGPGFGG-----MNRIG 325

Query: 412 NNTGSGGLNLLNNLNP SILA AVVGNLGNQG--GNLSNPLSSSSLS-----NLGLNLGN SG 463
 G GGL N +G G G G L ++SS+ ++GL+ G
 Sbjct: 326 GGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGHRDIGLSRGFGD 377

Query: 464 NDDNLPPSNVGLSNYSSGGTGGGNSYSSGNNYSGGGGSSN-----LGYNAYSSS-GG 515
 + L + +G +G G N G+ SGG GS N +G + SSS
 Sbjct: 378 SFGR LGSAMIG----GITGRIGSSNMGPVSGSGISGGMGSMNSVTGGMGMLDRMSSSFDR 433

Query: 516 MGGGNGGVGVDGNDYNTGNPLDVYGGGNSVGNVGSANAVGASRKSDTII IKNPITCT 575
 MG G G + D + G G G +GS K + I ++N+P T
 Sbjct: 434 MGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLT 482

Query: 576 WQTLRDKPREIGDVKFAEI-----RGNDVGVVRFFKERDAELALALMDGSRLDGRNIKV 629
 WQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 483 WQKLKEKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 541

Score = 68.6 bits (166), Expect = 2e-10
Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGAGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +
Sbjct: 437 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 492

Query: 80 IVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEKMNRVEVNGRELVVKED 133
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 493 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLD 544

Score = 55.5 bits (132), Expect = 2e-06
Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 11/157 (7%)

Query: 152 GGGGGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNY 211
G G G+ GG G N GG G +D F R G ++ + +
Sbjct: 400 GPVGSISGGMGSMNSVTGGMGMG-LDRMSSSFDRM-----GPGIGAILERSIDMDRGF 452

Query: 212 NLYGLSASFLESGLISGPLHNKVFVANLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNS 271
+ + E +G G N++FV NL + + +KLK+ F G V ++ ++ G S
Sbjct: 453 LSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKLKEKFSQCGHVMFAEIKMEN-GKS 508

Query: 272 RGFVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
+G + +D P A +A +++ + R + VRLDR
Sbjct: 509 KGCCTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 545

Figure 15B. Multiple Sequence Alignment (ClustalW 1.83)

```

CG9373 Dm -----
KIAA1341 Hs PLSRSEPLSSGGRGGGSGGGMADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK
MyEF-2 Hs -----
FLJ13071 Hs -----MADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK

CG9373 Dm ---MSMDASNSVESREKERDRRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNC
KIAA1341 Hs QQPQHSSSSNGVKMENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN
MyEF-2 Hs -----MENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN
FLJ13071 Hs QQPQHSSSSNGVKMENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN

CG9373 Dm RVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEK
KIAA1341 Hs RVFISNIPYDMKWQAIKDLMKREKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKALET
MyEF-2 Hs RVFISNIPYDMKWQAIKDLMKREKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKALET
FLJ13071 Hs RVFISNIPYDMKWQAIKDLMKREKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKALET

CG9373 Dm MNRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDHM
KIAA1341 Hs MNKYDLSGRPLNIKEDPDGENARR-----ALQRTGGSFPGGHVPDMGSG-----
MyEF-2 Hs MNKYDLSGRRVNIKEDPDGENARR-----ALQRTGTSFQGSASDVGSG-----
FLJ13071 Hs MNKYDLSGRPLNIKEDPDGENARR-----ASQRTGGSFPGGHVPDMGSG-----

CG9373 Dm DDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVA
KIAA1341 Hs -----LMNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA
MyEF-2 Hs -----LVNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA
FLJ13071 Hs -----LMNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA

```

CG9373 Dm NLDYKVDNKKLKQVFKLAGKVQSVDLSDKEGNSRGFAVIEYDHPVEAVQAI SMLDRQML
 KIAA1341 Hs NLDKFKVGWKKLKEVFSIAGTVKRADIKEDKD GKSRGMGTVTTFEQAI EAVQAI SMFNGQFL
 MyEF-2 Hs NLDKFKVGWKKLKEVFSIAGTVKAGSYKEDKD GKSRGMGTVTTFEQAI EAVQAI SMFNGQFL
 FLJ13071 Hs NLDKFKVGWKKLKEVFSIAGTVKRADIKEDKD GKSRGMGTVTTFEQAI EAVQAI SMFNGQFL

CG9373 Dm FDRRMTVRLDRI PDKN EGIK-----LPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQS
 KIAA1341 Hs FDRPMHVKMDDKSVPHEEYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----
 MyEF-2 Hs FDRPMHVKMDDKSVPHEEYRSPDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----
 FLJ13071 Hs FDRPMHVKMDDKSVPHEEYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----

CG9373 Dm QQQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTG-VMFGNHA AVQPSVAPVQKP
 KIAA1341 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
 MyEF-2 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
 FLJ13071 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----

CG9373 Dm SLGNNTGSGGLN LNNLNP SILAAVVGNLGNQGGNLSNPL LSSSLSNLGLNLGNSGNDNL
 KIAA1341 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRLGSAM-IGGFAGRI
 MyEF-2 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGHRD IGLSRGFGDSFGRLGSAM-IGGITGRI
 FLJ13071 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRLG-----

CG9373 Dm PPSNVGLSN NYSSGGTGGGNSYSSGNNYSGGGSSNLGYNAYSSSGMGGGNGGVGDGN
 KIAA1341 Hs GSSNMGPVGSGISGGMGSMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI
 MyEF-2 Hs GSSNMGPVGSGISGGMGSMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI
 FLJ13071 Hs -----GGMGGMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI

CG9373 Dm DYNTGNPLDVYGGG SNVGSN VGSANAVGASRKS DTII IKNVPITCTWQTL RDKFREIGD
 KIAA1341 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH
 MyEF-2 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH
 FLJ13071 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH

CG9373 Dm VKFAEIRGND-----VGVRFFKERDAELAI ALMDGSRLDGRNIKVTYF---
 KIAA1341 Hs VMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDRNA
 MyEF-2 Hs VMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDRNA
 FLJ13071 Hs VMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDRNA

Figure 16. Expression of CG9373 Homologs in Mammalian Tissues

Figure 16A. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in wild type mouse tissues (DCt Pancreas = 20,90)

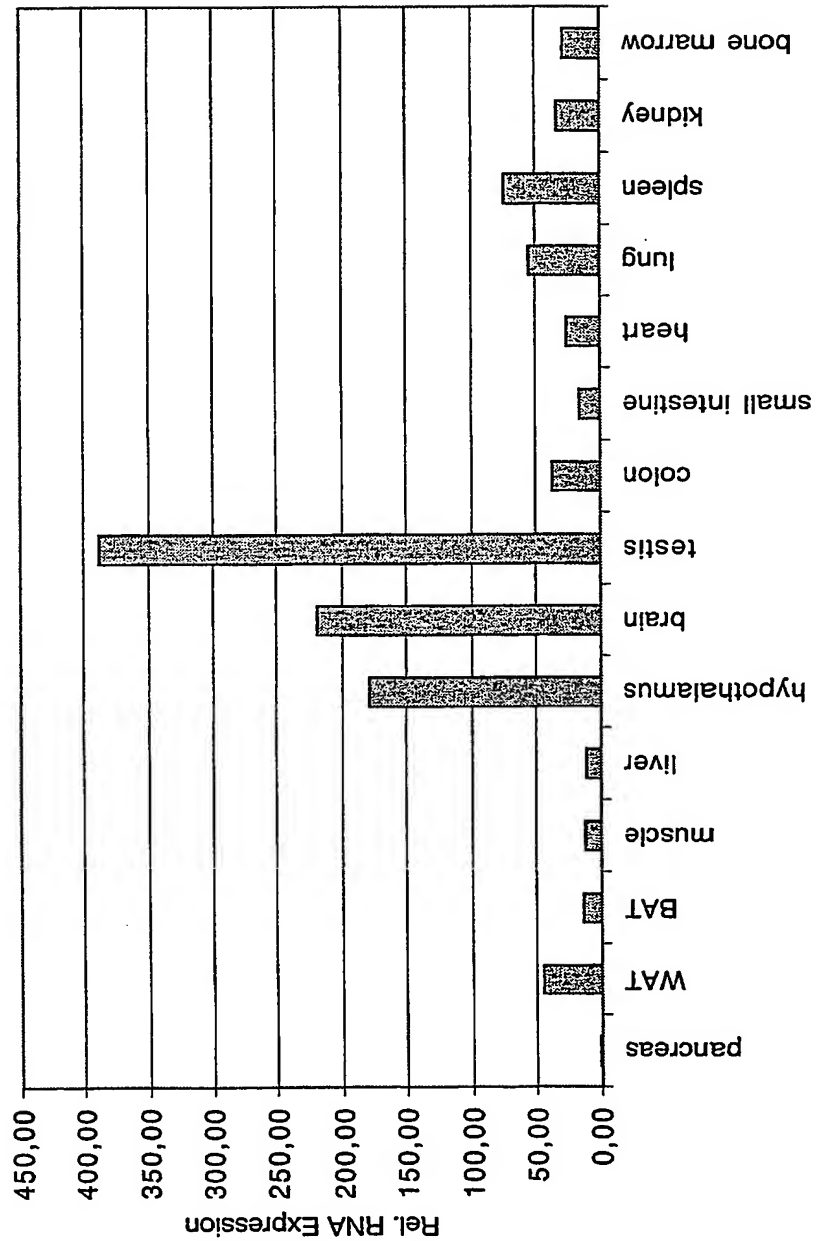


Figure 16B. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in different mouse models

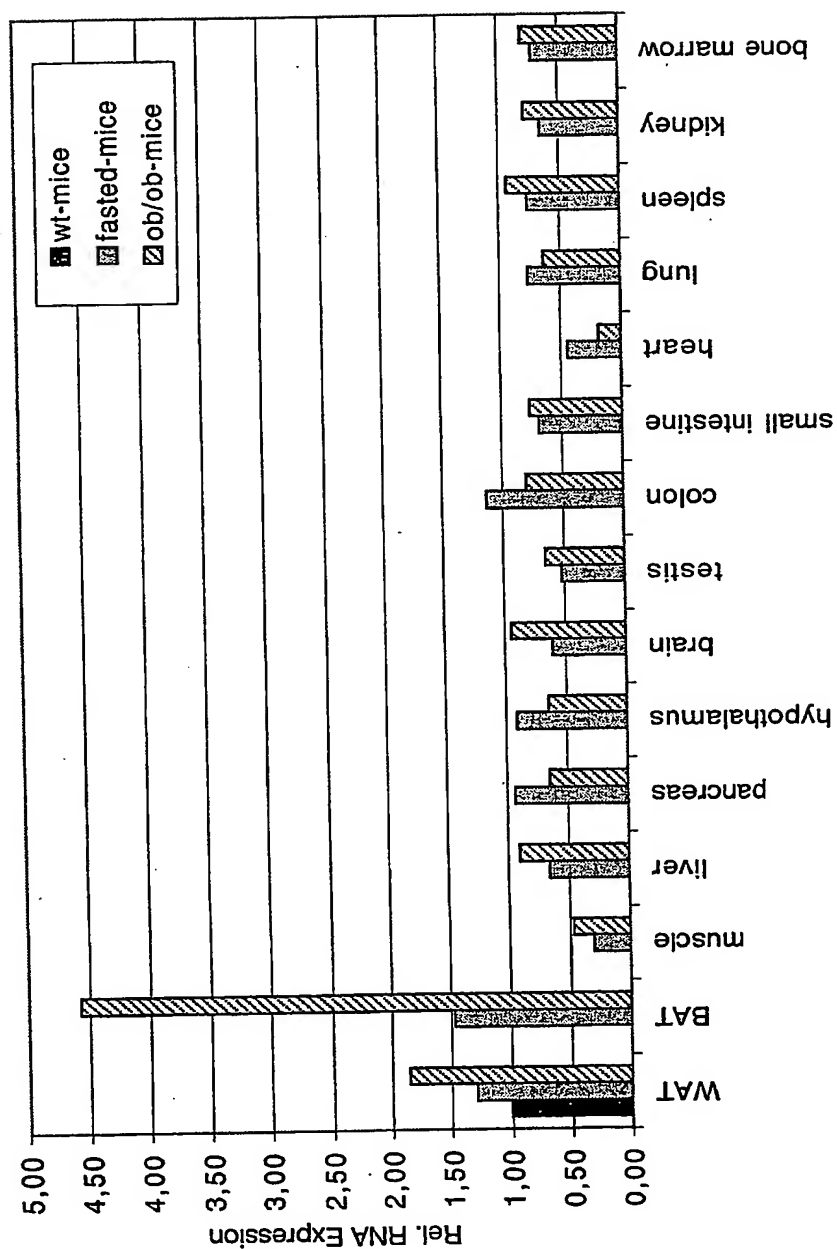


Figure 16C. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in mice fed with a high fat diet compared to mice fed with a standard diet

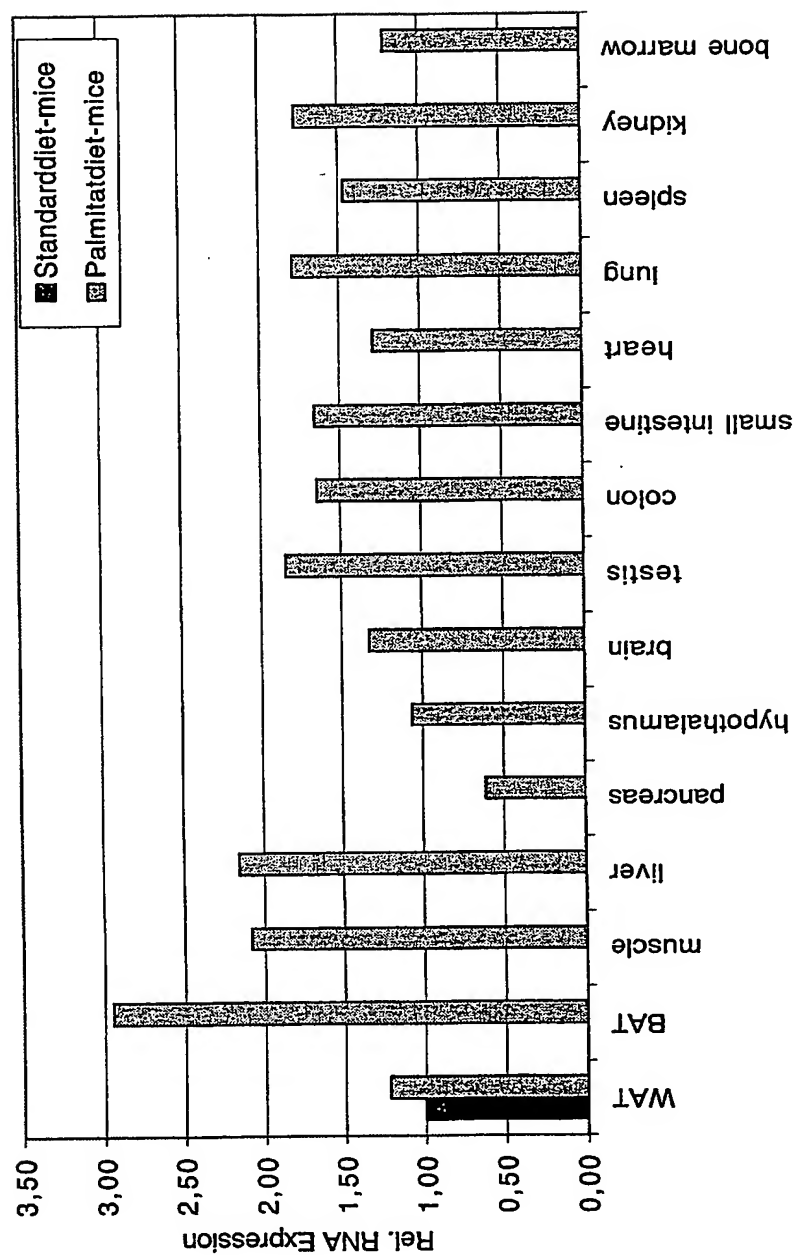


Figure 17. Triglyceride content of a *Drosophila cpo* (GadFly Accession Number CG18434) mutant

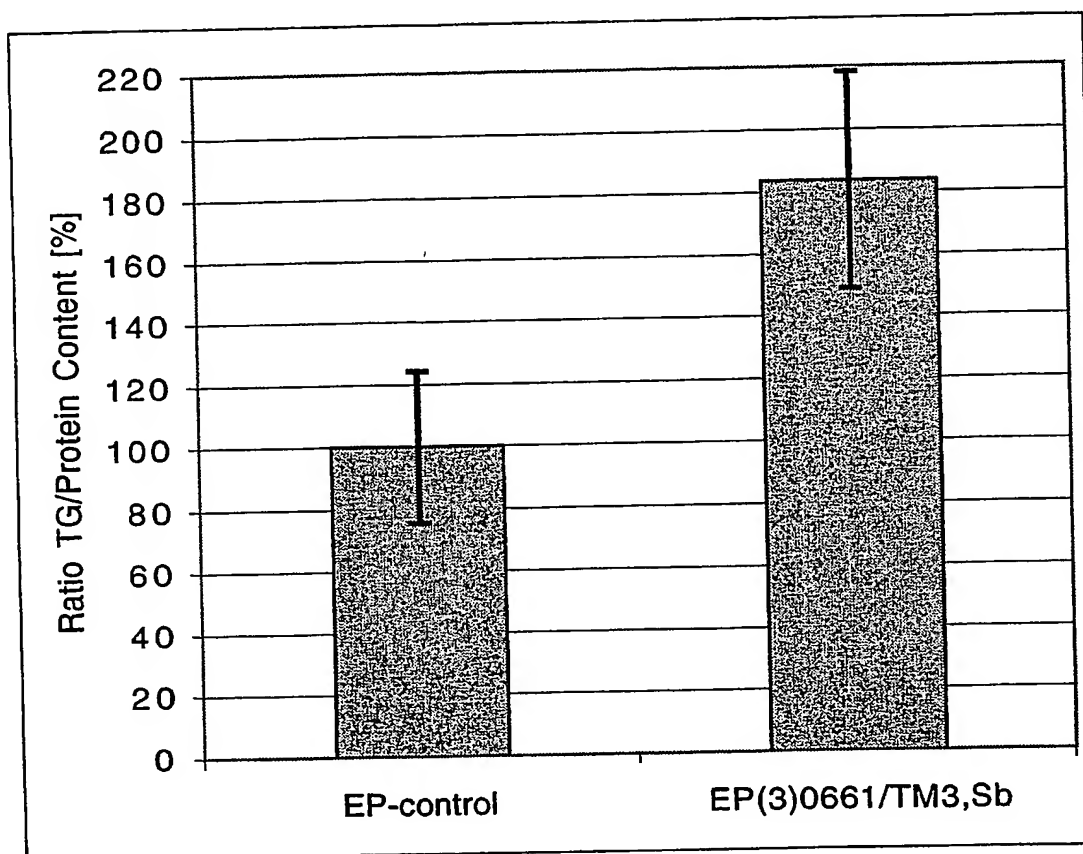


Figure 18. Molecular organisation of the *cpo* gene (GadFly Accession Number CG18434)

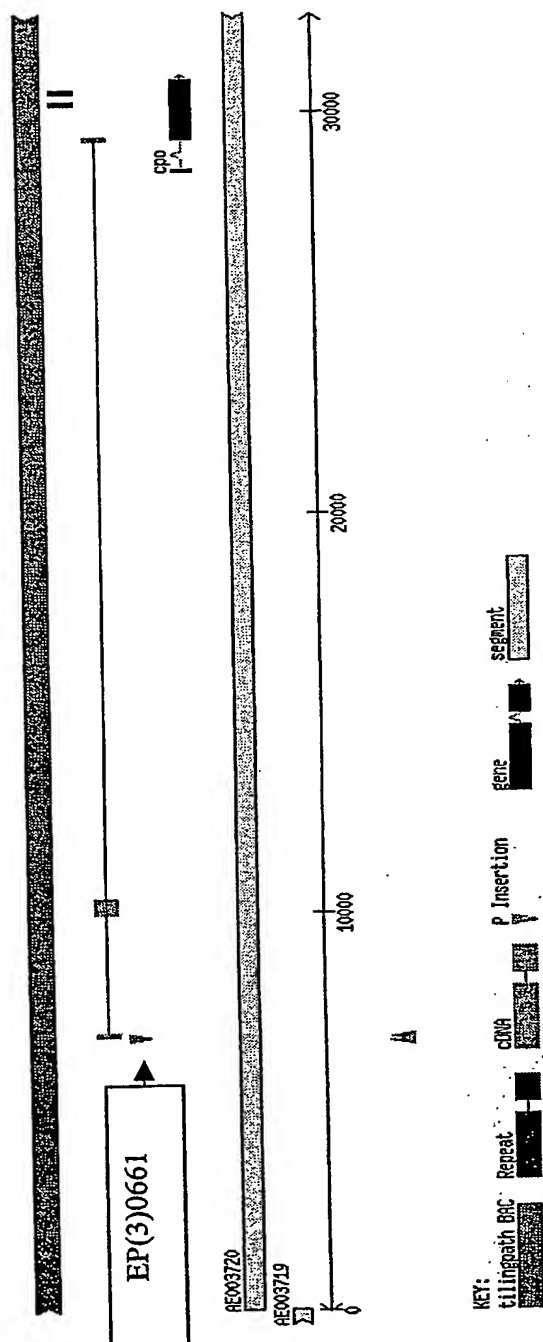


Figure 19. Homology of *Drosophila cpo* (GadFly Accession Number CG31243 and CG18434) to human RNA binding proteins with multiple splicing

Figure 19A. Multiple Sequence Alignment (ClustalW 1.83)

```

cpo Dm      LVKIAN YQDLLGSHHQLLIAATAAAAAAAAAAEPQLQLQHLLPAAPTTPAVISNPINSIGP
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      INQISSSSHPSNNNQAVFEKAITISSIAIKRRPTLPQTPASAPQVLSPPKRCQAAAVS
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      VLPVTVFPVPVPSVPLPVSVFPVSVKGHPISTHQIAHTHQISHSHPISTHPHHHQLSFA
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      HPTQFAAAVAAHHQQQQQQQAQQQQQAVQQQQQQAVQQQQVAYAVAASPOLQQQQQQQQQH
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      RLAQFNQAAAAALLNQHLQQQHQAQQQQHQAQQQSLAHYGGYQLHRYAPQQQQQHILLSS
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      GSSSSKHNSNNNSNTSAGAASAAVPIATSVAAVPTTGGSLPDSPAHESSHESNSATASA
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      PTTSPAGSVTSAAPTATATAAAAGSAAATAAATGTPATSAVSDSNNNNLNSSSSSNSNSN
NP_006858 Hs -----
IPI00161102 Hs -----MNNGGK

cpo Dm      AIMENQMALAPLGLSQSMDSVNTASNEEEVRTL FVSGLPMDAKPRELYLLFRAYEGYEGS
NP_006858 Hs AEKENTPSEANL-----QEEEVRTL FVSGLPLDIKPRELYLLFRPFKGYEGS
IPI00161102 Hs -----QVRTLFVSGLPVDIKPRELYLLFRPFK-----

cpo Dm      LLKVT SKNGKTASPVGFVTFHTRAGAEAAKQDLQGVRFDPDMPQTIRLEFAKSNTKVSKP
NP_006858 Hs LIKLT SKQ-----PVGFVSFDSRSEAEAAKNALNGIRFDPEIQTLRLEFAKANTKMAKN
IPI00161102 Hs -----PVGFVIFDSRAGAEAAKNALNGIRFDPENPQTLRLEFAKANTKMAKS

cpo Dm      KPQPN TATTASHPALMHPLTG-----HLGGPFFPGGPPELWHHPLAYSAAAAAELPG-----
NP_006858 Hs KLVGTPNPSTPLPNTVPQFIAREPYELTVPALYPSSPEVWAPYPLYPALAPALPPPAFT
IPI00161102 Hs KL MATPNPSNVHPALGAHFIARDPYDLMGAALIPASPEAWAPYPLYTTELTPAISHAAFT

cpo Dm      -----AAALQHATLVHPALHPQVP---VRSYL
NP_006858 Hs YP-----ASLHAQMRWLPPSEATSQGWKSRQFC
IPI00161102 Hs YPTATAAAALHAQVRWYPSSDTTQGWKYRQFC

```


FIGURE 19B. Amino acid sequence encoded by Drosophila gene CG31243 (GadFly Accession Number), SEQ ID NO:1

>CG31243-PA (AE003720) [gene_syn=CG31243] [prot_desc=CG31243 gene product from transcript CG31243-RA]

```
1  LVKIANVQDL  LGSHHQLLIA  ATAAAAAAAA  AEPQLQLQHL  LPAAPTTPAV  ISNPINSIGP
61  INQISSSSHP  SNNNQAVFE  KAITISSIAI  KRRPTLPQTP  ASAPQVLSPS  PKRQCAAASV
121 VLPVTVVPV  PVSVPPLPVS  PVPVSVKGHP  ISHTHQIAHT  HQISHSHPI  HPHHHQLSFA
181 HPTQFAAAVA  AHHQHQHQHQ  AQQQQQAVQQ  QQQQAVQQQQ  VAYAVAASPQ  LQQQQQQQQH
241 RLAQFNQAAA  AALLNQHLQQ  QHQHQHQHQ  AQQQSLAHYG  GYQLHRYAPQ  QQQQHILLSS
301 GSSSSKHNSN  NNSNTSAGAA  SAAVPIATSV  AAVPTTGGSL  PDSPAHEHS  HESNSATASA
361 PTPSPAGSV  TSAAPTATAT  AAAAGSAAAT  AAATGTPATS  AVSDSNNNLN  SSSSNSNSN
421 AIMENQMALA  PLGLSQSMDS  VNTASNEEEV  RTLFVSGLEP  DAKPRELYLL  FRAYEGYEGS
481 LLKVTSKNGK  TASPVGFTF  HTRAGAEAAK  QDLQGVRFDP  DMPQTIRLEF  AKSNTKVSKP
541 KPQPNTATTA  SHPALMHPLT  GHLGGPFFPG  GPELWHHPLA  YSAAAAAELP  GAAALQHATL
601 VHPALHPQVP  VRSYL
```

Figure 20. Expression of a human *cpo* homolog in mammalian (human) tissue

Quantitative analysis of RNA binding protein with multiple splicing (RBPMS) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

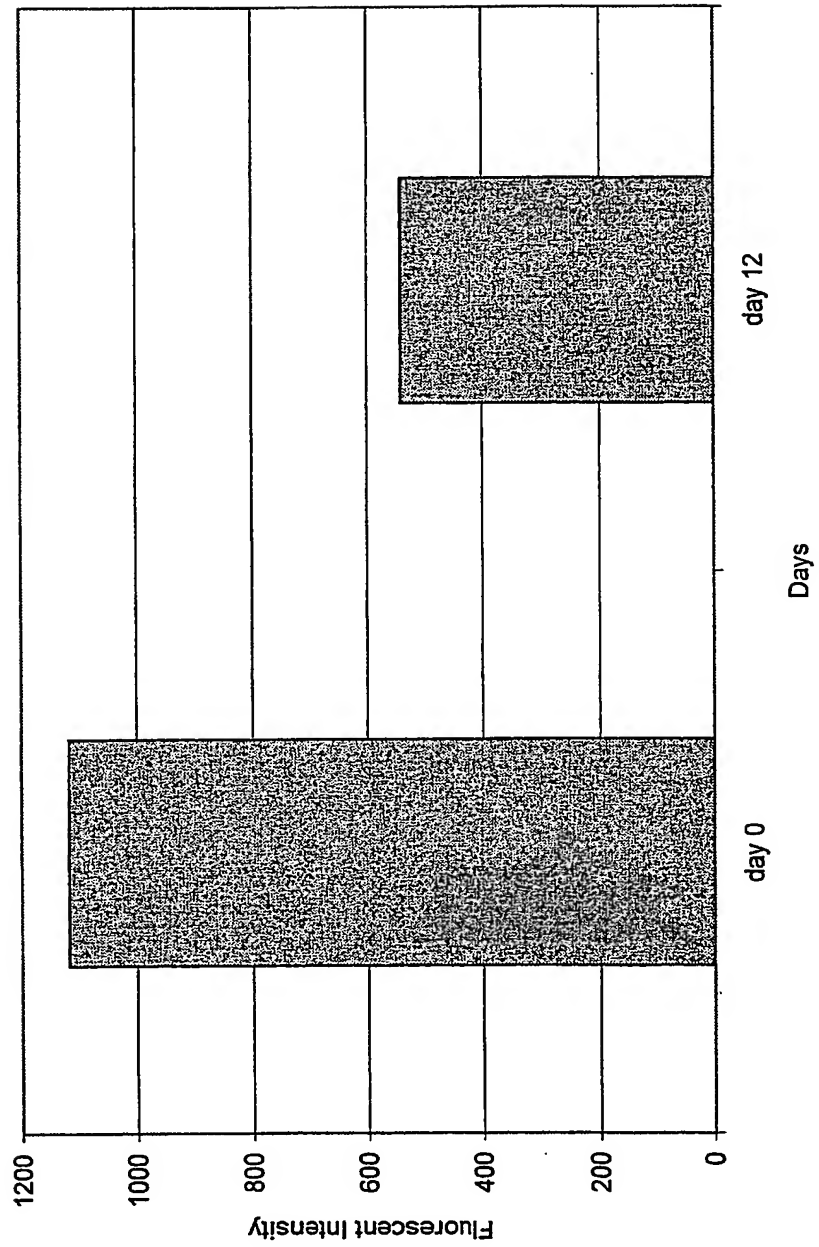


Figure 21. Triglyceride content of a *Drosophila Jafrac1* (GadFly Accession Number CG1633) mutant

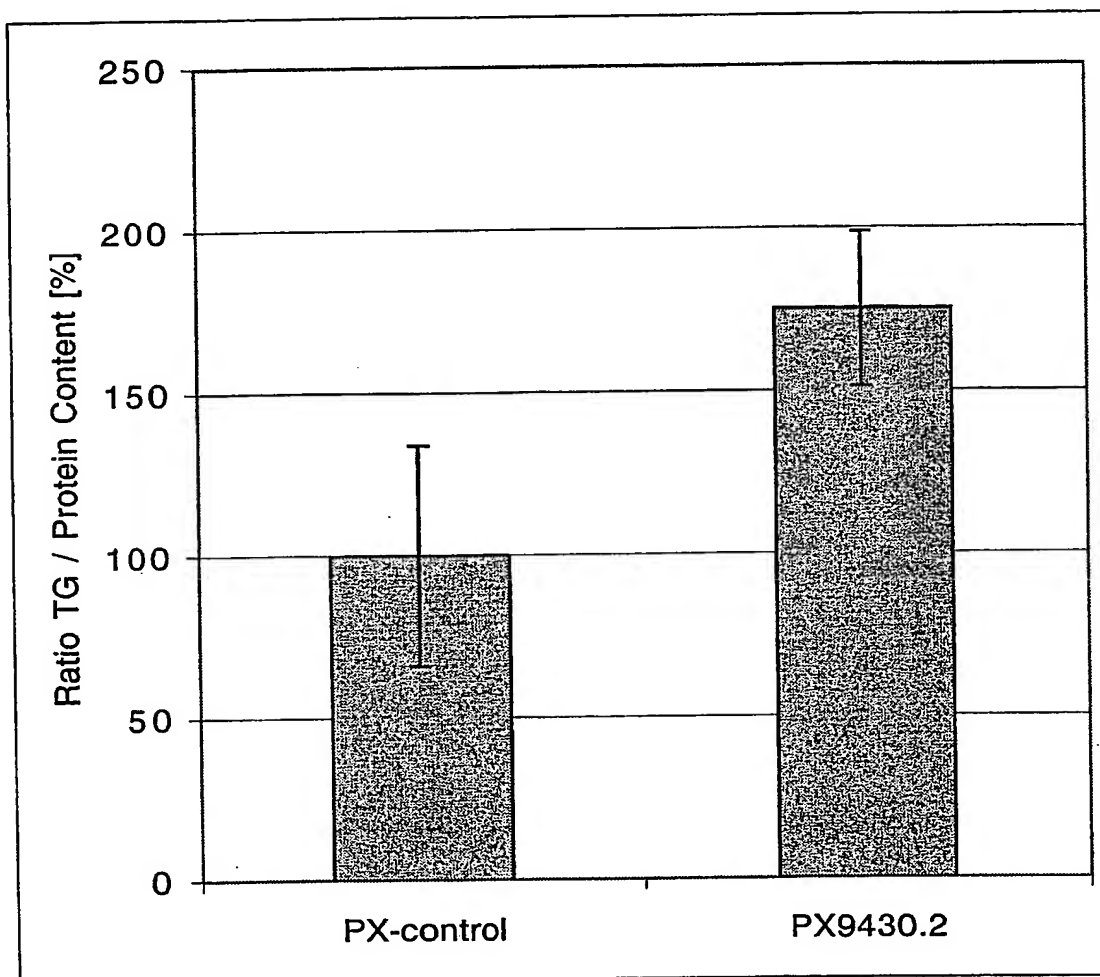


Figure 22. Molecular organisation of the *Jafracl* gene (GadFly Accession Number CG1633)

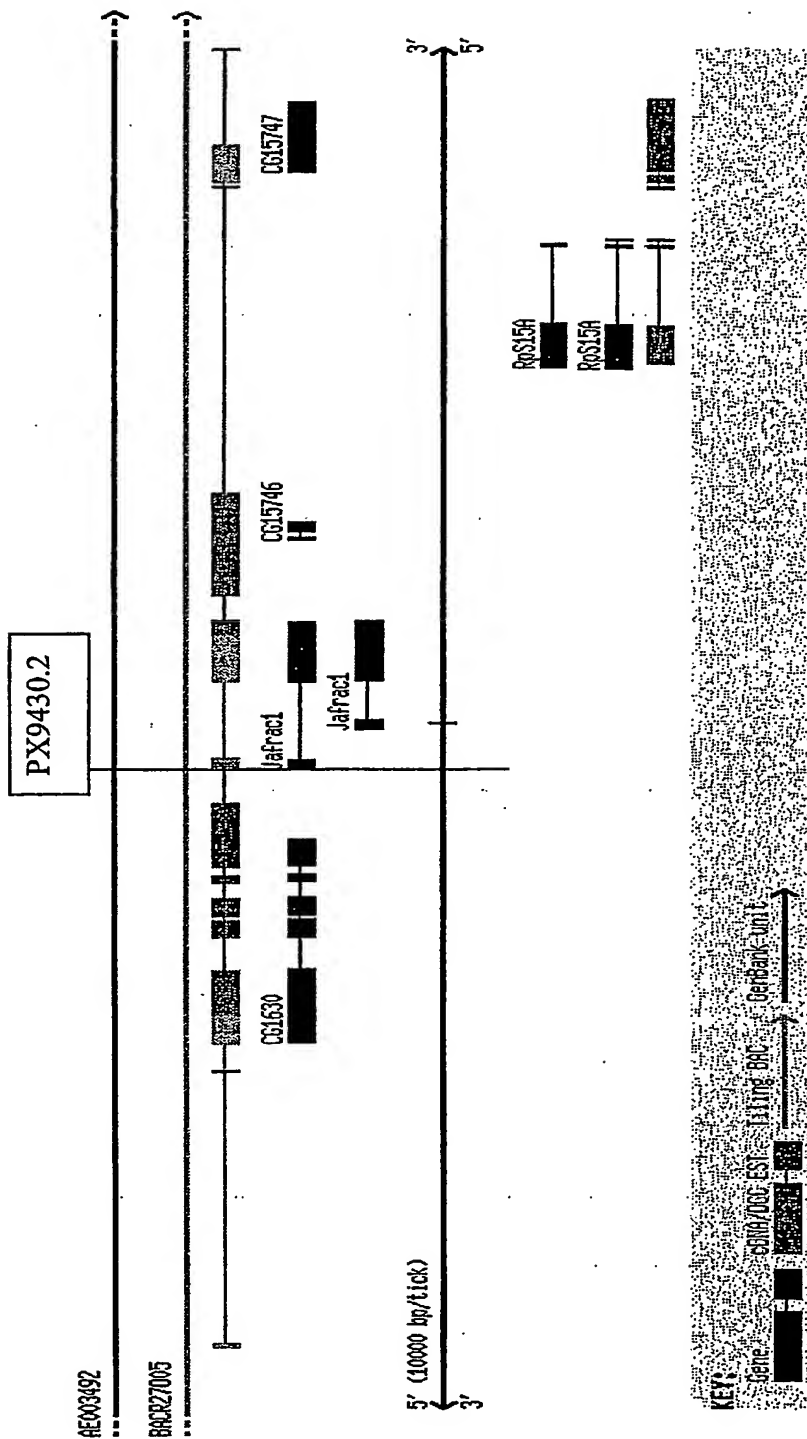


Figure 23. Homology of *Drosophila Jafrac1* (GadFly Accession Number CG1633) to human peroxiredoxin 1 and human peroxiredoxin 2 (similar to peroxiredoxin 1)

Figure 23A. BLASTP results for *Jafrac1*

Homology to human protein XP_009063.2 (GenBank Accession Number)

ref|XP_009063.2| (XM_009063) peroxiredoxin 2 [Homo sapiens]
Length = 198

Score = 283 bits (723), Expect = 9e-76
Identities = 134/188 (71%), Positives = 157/188 (83%)

```
Query: 3   QLQKPAPAFAGTAVVNGVFKDIKLSDYKGKYLVLFFYPPLDFTFVCPTEIIAFSESAAEFR 62
          ++ KPAP F TAVV+G FK++KLSDYKGKY+VLFFYPPLDFTFVCPTEIIAFS A +FR
Sbjct: 7   RIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPPLDFTFVCPTEIIAFSNRAEDFR 66

Query: 63  KINCEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDIPLLADKSMKVARDYGVLDDEETGIPF 122
          K+ CEV+G S DSQFTHLAWINTPRK+GGLG ++IPLLAD + +++ DYGV L + GI +
Sbjct: 67  KLGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEYGV LKTDEGIAY 126

Query: 123 RGLFIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPQKTMVAD 182
          RGLFIID K LRQITVNDLPVGRSV+E LRLVQAFQYTD++GEVCPA WKPG T+ +
Sbjct: 127 RGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTD EHGVECPAGWKPGSDTIKPN 186

Query: 183 PTKSKEYF 190
          SKEYF
Sbjct: 187 VDDSKEYF 194
```

Homology to human protein NP_002565.1 (GenBank Accession Number)

ref|NP_002565.1| (NM_002574) peroxiredoxin 1; Proliferation-associated gene A;
proliferation-associated gene A (natural killer-enhancing factor A) [Homo sapiens]
ref|XP_001393.2| (XM_001393) peroxiredoxin 1 [Homo sapiens]
Length = 199

Score = 281 bits (718), Expect = 3e-75
Identities = 135/185 (72%), Positives = 154/185 (82%), Gaps = 1/185 (0%)

```
Query: 7   PAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFFYPPLDFTFVCPTEIIAFSESAAEFRKIN 65
          PAP F TAV+ +G FKDI LSDYKGKY+V FFYPPLDFTFVCPTEIIAFS+ A EF+K+N
Sbjct: 11  PAPNFKATAVMPDGQFKDISLSDYKGKYVVFVFFYPPLDFTFVCPTEIIAFSDRAEEFKLN 70

Query: 66  CEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDIPLLADKSMKVARDYGVLDDEETGIPFRGL 125
          C+VIG S DS F HLA W+NTP+KQGGLG M+IPL++D +A+DYGV L + GI FRGL
Sbjct: 71  CQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGV LKADEGISFRGL 130

Query: 126 FIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPQKTMVADPTK 185
          FIIDDK LRQITVNDLPVGRSV+ETLRLVQAFQ+TDK+GEVCPA WKPG T+ D K
Sbjct: 131 FIIDDKGILRQITVNDLPVGRSVDET LRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK 190

Query: 186 SKEYF 190
          SKEYF
Sbjct: 191 SKEYF 195
```

Figure 23B. Multiple Sequence Alignment (ClustalW 1.83)

Jafrac1 Dm MP----QLQKPAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTETIIAFS
PRDX1 Hs MSSGNAKIGHAPAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPTETIIAFS
PRDX2 Hs MASGNARIGKPAPDFKATAVV-DGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTETIIAFS

Jafrac1 Dm ESAAEFRKINCEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDPLLADKSMKVARDYGVLD
PRDX1 Hs DRAEEFKKLNCQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLK
PRDX2 Hs NRAEDFRKLGCEVLGVSVDQSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLK

Jafrac1 Dm EETGIPFRGLFIIDDKQNLRQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPG
PRDX1 Hs ADEGISFRGLFIIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPG
PRDX2 Hs TDEGIAYRGLFIIDGKGVLRLQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPG

Jafrac1 Dm QKTMVADPTKSKEYFETTS
PRDX1 Hs SDTIKPDVQKSKEYFSKQK
PRDX2 Hs SDTIKPNVDDSKEYFSKHN

Figure 24. Expression of a human *Jafracl* homolog in mammalian (human) tissue
Quantitative analysis of Peroxiredoxin 1 (PRDX1) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

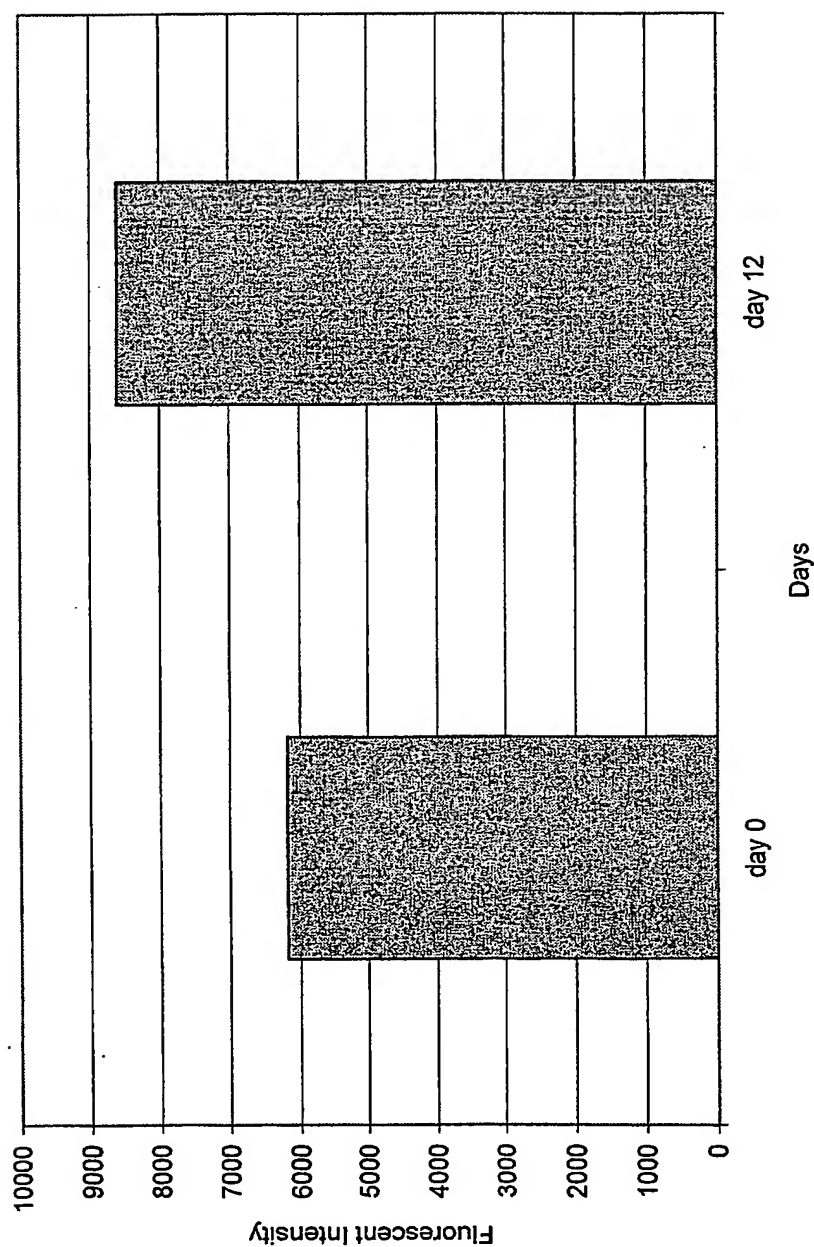


Figure 25. Triglyceride content of a *Drosophila* CG14440 (GadFly Accession Number) mutant

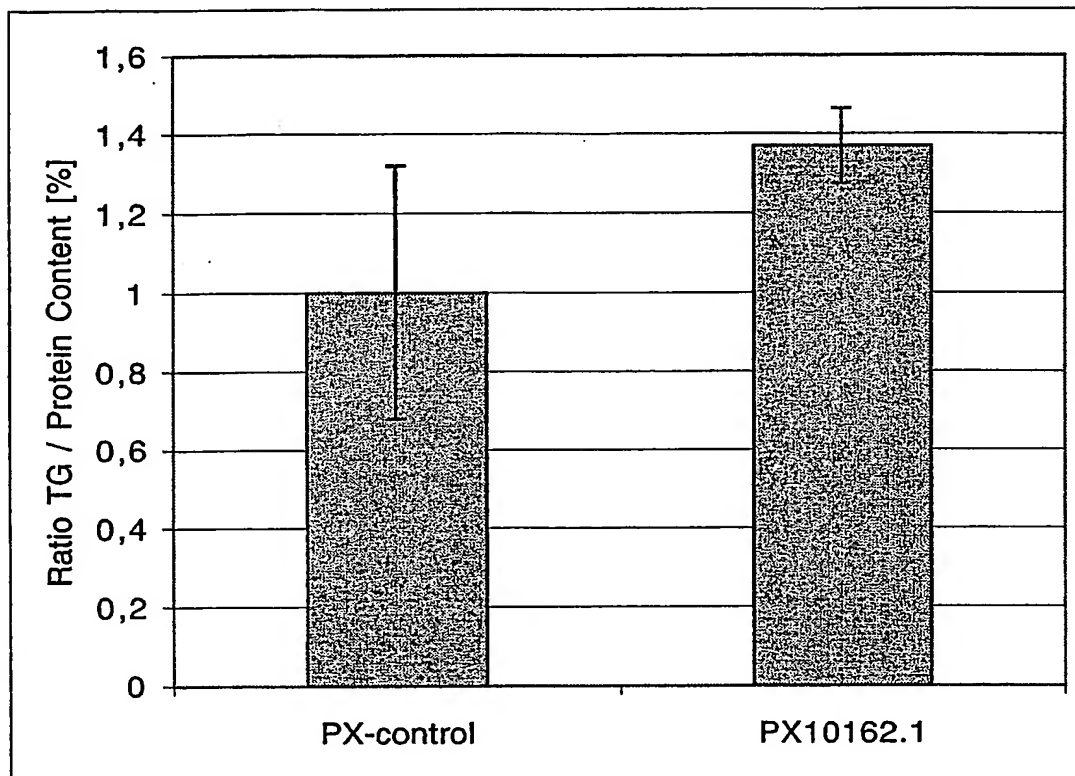


Figure 26. Molecular organization of the CG14440 gene (GadFly Accession Number)

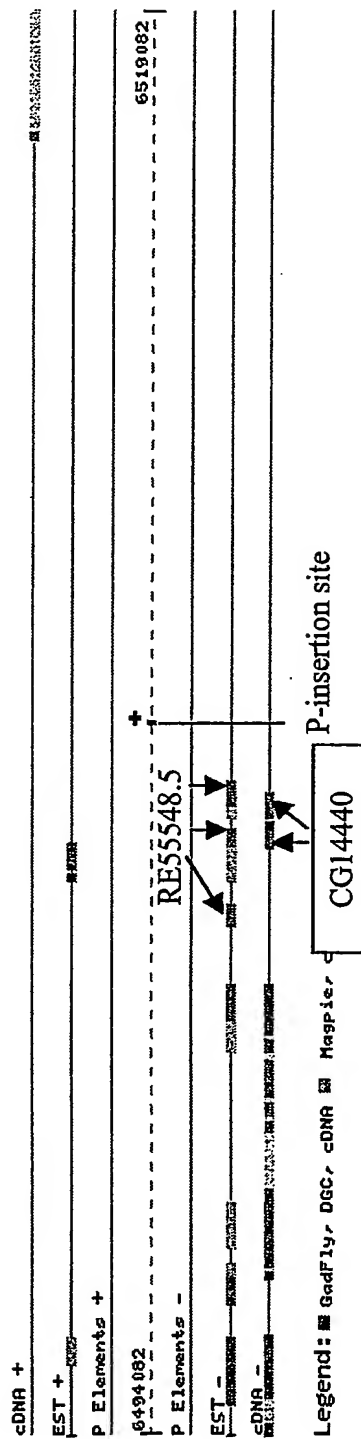


Figure 27. BLASTP results for CG14440 (GadFly Accession Number)**Homology to human protein NP_060000.1 (GenBank Accession Number)**

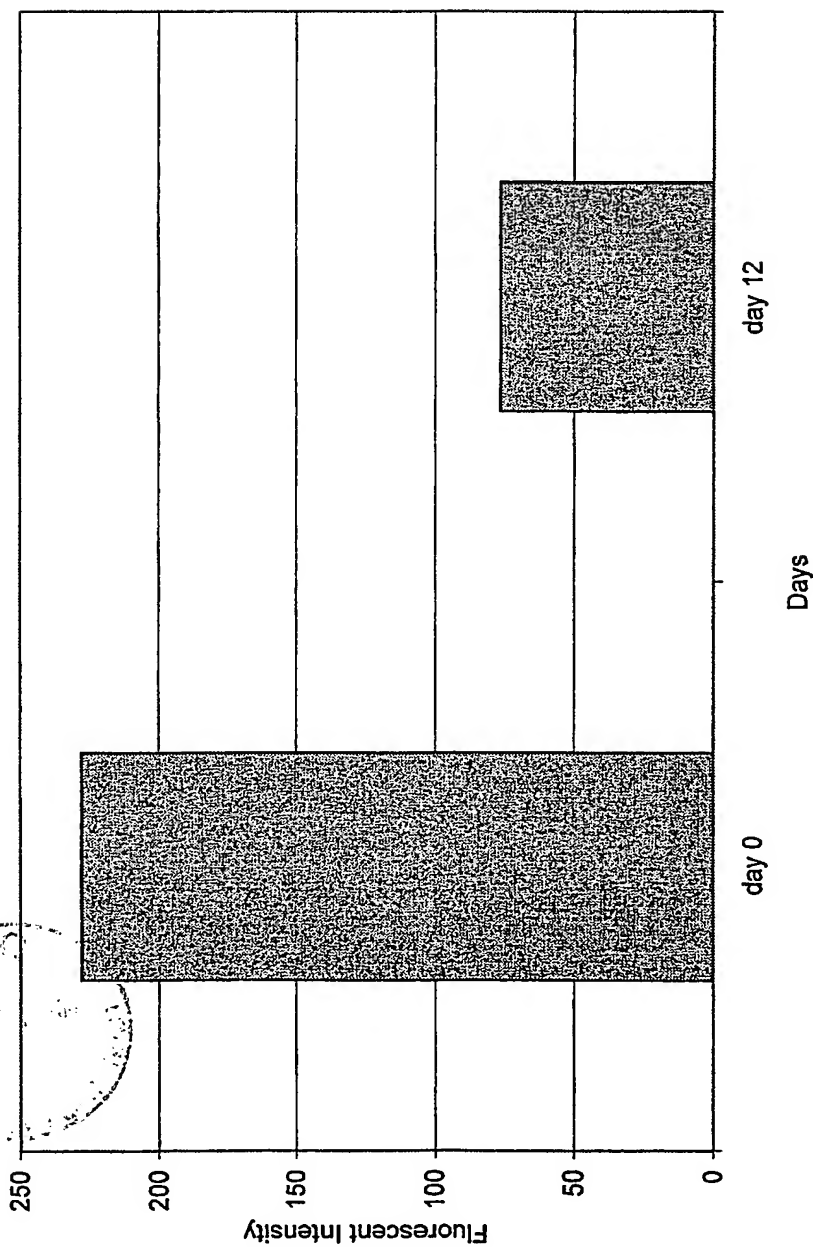
ref|NP_060000.1| (NM_017530) hypothetical protein LOC55565 [Homo sapiens]
Length = 370

Score = 77.4 bits (189), Expect = 2e-13
Identities = 41/106 (38%), Positives = 62/106 (57%)

Query: 195 QGQSSRAQKAARRRSNESIEARERRLERNAARMRDKRASEAEYRVRLAKNAEANRVRR 254
+ Q+ +K A RR NE +E R +RLER + +R E+ E VR ++ EA R++R
Sbjct: 207 EAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDNETPEEREVRRMRDREAKRLQR 266

Query: 255 QNETEVQRTLRLMKNAARQRLRRASETVEERKKRLAKAAERMRIAR 300
ET+ QR RL ++ RL+RA+ET E+R+ RL + E R+ R
Sbjct: 267 MQETDEQRARRLQDRREAMRLKRANETPEKRQARLIREREAKRLKR 312

Figure 28. Expression of the human CG14440 homolog in mammalian (human) tissue
Quantitative analysis of human hypothetical protein LOC55565 expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes



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